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APPLICATION FOR UNITED STATES PATENT

MULTI-FUNCTIONAL HEMATOPOIETIC FUSION PROTEINS BETWEEN SEQUENCE REARRANGED G-CSF RECEPTOR AGONISTS AND OTHER HEMATOPOIETIC FACTORS

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MULTI-FUNCTIONAL HEMATOPOIETIC FUSION PROTEINS BETWEEN SEQUENCE REARRANGED G-CSF RECEPTOR AGONISTS AND OTHER HEMATOPOIETIC FACTORS

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] The present application is a continuation of U.S. Pat. App. Ser. No. 09/510,238, filed February 22, 2002, pending, which is a divisional of U.S. Pat. App. Ser. No. 08/835,162 filed April 4, 1997, now issued as U.S. Pat. No. 6,066,318 on May 23, 2000, which is a continuation-in-part of PCT/US 96/15774 filed October 4, 1996 which claims priority under 35 U.S.C. §119(e) of U.S. Provisional Pat. App. Ser. No. 60/004,834, filed October 5, 1995, now abandoned.

REFERENCE TO A "SEQUENTIAL LISTING," A TABLE, OR A COMPTUER PROGRAM LISTING APPENDIX SUBMITTED ON A DISKETTE

[0002] This application includes a computer program listing appendix, pursuant to 37 CFR 1.96, contained on a diskette, which is incorporated fully into this application by this reference.

The diskette is labeled as follows:

Applicant:	Feng, et al.
Title:	Multi-Functional Hematopoietic Fusion Proteins Between Sequence Rearranged G-CSF Receptor Agonists and Other Hematopoietic Factors
Recorded:	October 23, 2003
Atty No.:	126181-1058
Serial No.:	Unknown
Filing Date:	October 27, 2003

The diskette contains the following file in ASCII file format:

File Name	File size	Creation Date
Sequence.txt	574 kb	October 23, 2003

BACKGROUND OF THE INVENTION

[0003] The present invention relates to multi-functional hematopoietic receptor agonists.

[0004] Colony stimulating factors (CSFs) which stimulate the differentiation and/or proliferation of bone marrow cells have generated much interest because of their therapeutic potential for restoring depressed levels of hematopoietic stem cell-derived cells. CSFs in both human and murine systems have been identified and distinguished according to their activities. For example, granulocyte-CSF (G-CSF) and macrophage-CSF (M-CSF) stimulate the in vitro formation of neutrophilic granulocyte and macrophage colonies, respectively, while GM-CSF and interleukin-3 (IL-3) have broader activities and stimulate the formation of both macrophage, neutrophilic and eosinophilic granulocyte colonies. IL-3 also stimulates the formation of mast, megakaryocyte and pure and mixed erythroid colonies.

DESCRIPTION OF RELATED ART

[0005] U.S. 4,877,729 and U.S. 4,959,455 disclose human IL-3 and gibbon IL-3 cDNAs and the protein sequences for which

they code. The hIL-3 disclosed has serine rather than proline at position 8 in the protein sequence.

[0006] International Patent Application (PCT) WO 88/00598 discloses gibbon- and human-like IL-3. The hIL-3 contains a Ser^8 -> Pro^8 replacement. Suggestions are made to replace Cys by Ser, thereby breaking the disulfide bridge, and to replace one or more amino acids at the glycosylation sites.

[0007] U.S. 4,810,643 discloses the DNA sequence encoding human G-CSF.

[0008] WO 91/02754 discloses a fusion protein comprised of GM-CSF and IL-3 which has increased biological activity compared to GM-CSF or IL-3 alone. Also disclosed are nonglycosylated IL-3 and GM-CSF analog proteins as components of the multi-functional hematopoietic receptor agonist.

[0009] WO 92/04455 discloses fusion proteins composed of IL-3 fused to a lymphokine selected from the group consisting of IL-3, IL-6, IL-7, IL-9, IL-11, EPO and G-CSF.

[0010] WO 95/21197 and WO 95/21254 disclose fusion proteins capable of broad multi-functional hematopoietic properties.

[0011] GB 2,285,446 relates to the c-mpl ligand (thrombopoietin) and various forms of thrombopoietin which are shown to influence the replication, differentiation and

maturation of megakaryocytes and megakaryocytes progenitors which may be used for the treatment of thrombocytopenia.

[0012] EP 675,201 A1 relates to the c-mpl ligand (Megakaryocyte growth and development factor (MGDF), allelic variations of c-mpl ligand and c-mpl ligand attached to water soluble polymers such as polyethylene glycol.

[0013] WO 95/21920 provides the murine and human c-mpl ligand and polypeptide fragments thereof. The proteins are useful for *in vivo* and *ex vivo* therapy for stimulating platelet production.

REARRANGEMENT OF PROTEIN SEQUENCES

[0014] In evolution, rearrangements of DNA sequences serve an important role in generating a diversity of protein structure and function. Gene duplication and exon shuffling provide an important mechanism to rapidly generate diversity and thereby provide organisms with a competitive advantage, especially since the basal mutation rate is low (Doolittle, *Protein Science* **1**:191-200, 1992).

[0015] The development of recombinant DNA methods has made it possible to study the effects of sequence transposition on protein folding, structure and function. The approach used in creating new sequences resembles that of naturally occurring pairs of proteins that are related by linear reorganization of

their amino acid sequences (Cunningham, et al., *Proc. Natl. Acad. Sci. U.S.A.* **76**:3218-3222, 1979; Teather & Erfle, *J. Bacteriol.* **172**: 3837-3841, 1990; Schimming et al., *Eur. J. Biochem.* **204**: 13-19, 1992; Yamiuchi and Minamikawa, *FEBS Lett.* **260**:127-130, 1991; MacGregor et al., *FEBS Lett.* **378**:263-266). The first in vitro application of this type of rearrangement to proteins was described by Goldenberg and Creighton (*J. Mol. Biol.* **165**:407-413, 1983). A new N-terminus is selected at an internal site (breakpoint) of the original sequence, the new sequence having the same order of amino acids as the original from the breakpoint until it reaches an amino acid that is at or near the original C-terminus. At this point the new sequence is joined, either directly or through an additional portion of sequence (linker), to an amino acid that is at or near the original N-terminus, and the new sequence continues with the same sequence as the original until it reaches a point that is at or near the amino acid that was N-terminal to the breakpoint site of the original sequence, this residue forming the new C-terminus of the chain.

[0016] This approach has been applied to proteins which range in size from 58 to 462 amino acids (Goldenberg & Creighton, *J. Mol. Biol.* **165**:407-413, 1983; Li & Coffino, *Mol. Cell. Biol.* **13**:2377-2383, 1993). The proteins examined have represented a broad range of structural classes, including

proteins that contain predominantly a-helix (interleukin-4; Kreitman et al., *Cytokine* **7**:311-318, 1995), b-sheet (interleukin-1; Horlick et al., *Protein Eng.* **5**:427-431, 1992), or mixtures of the two (yeast phosphoribosyl anthranilate isomerase; Luger et al., *Science* **243**:206-210, 1989). Broad categories of protein function are represented in these sequence reorganization studies:

Enzymes

T4 lysozyme	Zhang et al., *Biochemistry* **32**:12311-12318, 1993; Zhang et al., *Nature Struct. Biol.* **1**:434-438 (1995).
dihydrofolate reductase	Buchwalder et al., *Biochemistry* **31**:1621-1630, 1994; Protasova et al., *Prot. Eng.* **7**:1373-1377, 1995).
ribonuclease T1	Mullins et al., *J. Am. Chem. Soc.* **116**:5529-5533, 1994; Garrett et al., *Protein Science* **5**:204-211, 1996).
Bacillus b-glucanse	Hahn et al., *Proc. Natl. Acad. Sci.U.S.A.* **91**:10417-10421, 1994).
aspartate transcarbamoylase	Yang & Schachman, *Proc. Natl. Acad. Sci. U.S.A.* **90**:11980-11984, 1993).
phosphoribosyl anthranilate	Luger et al., *Science* **243**:206-210 (1989; Luger et al., *Prot. Eng.* Isomerase **3**:249-258, 1990).
pepsin/pepsinogen	Lin et al., *Protein Science* **4**:159-166, 1995).
glyceraldehyde-3-phosphate dehydrogenase	Vignais et al., *Protein Science* **4**:994-1000, 1995).
ornithine	Li & Coffino, *Mol. Cell. Biol.*

	decarboxylase **13**:2377-2383, 1993).
yeast phosphoglycerate dehydrogenase	Ritco-Vonsovici et al., *Biochemistry* **34**:16543-16551, 1995).
	Enzyme Inhibitor
basic pancreatic trypsin inhibitor	Goldenberg & Creighton, *J. Mol. Biol.* **165**:407-413, 1983).
	Cytokines
interleukin-1b	Horlick et al., *Protein Eng.* **5**:427-431, 1992).
interleukin-4	Kreitman et al., *Cytokine* **7**:311-318, 1995).
	Tyrosine Kinase Recognition Domain
a-spectrin SH3 domain	Viguera, et al., *J. Mol. Biol.* **247**:670-681, 1995).
	Transmembrane Protein
omp A	Koebnik & Krämer, *J. Mol. Biol.* **250**:617-626, 1995).
	Chimeric Protein
interleukin-4—*Pseudomonas* exotoxin	Kreitman et al., *Proc. Natl. Acad. Sci. U.S.A.* **91**:6889-6893, 1994).

[0017] The results of these studies have been highly variable. In many cases substantially lower activity, solubility or thermodynamic stability were observed (*E. coli* dihydrofolate reductase, aspartate transcarbamoylase, phosphoribosyl anthranilate isomerase, glyceraldehyde-3-phosphate dehydrogenase, ornithine decarboxylase, omp A, yeast

phosphoglycerate dehydrogenase). In other cases, the sequence rearranged protein appeared to have many nearly identical properties as its natural counterpart (basic pancreatic trypsin inhibitor, T4 lysozyme, ribonuclease T1, Bacillus b-glucanase, interleukin-1b, a-spectrin SH3 domain, pepsinogen, interleukin-4). In exceptional cases, an unexpected improvement over some properties of the natural sequence was observed, e.g., the solubility and refolding rate for rearranged a-spectrin SH3 domain sequences, and the receptor affinity and anti-tumor activity of transposed interleukin-4—Pseudomonas exotoxin fusion molecule (Kreitman et al., *Proc. Natl. Acad. Sci. U.S.A.* **91**:6889-6893, 1994; Kreitman et al., *Cancer Res.* **55**:3357-3363, 1995).

[0018] The primary motivation for these types of studies has been to study the role of short-range and long-range interactions in protein folding and stability. Sequence rearrangements of this type convert a subset of interactions that are long-range in the original sequence into short-range interactions in the new sequence, and vice versa. The fact that many of these sequence rearrangements are able to attain a conformation with at least some activity is persuasive evidence that protein folding occurs by multiple folding pathways (Viguera, et al., *J. Mol. Biol.* **247**:670-681, 1995). In the case of the SH3 domain of a-spectrin, choosing new

termini at locations that corresponded to b-hairpin turns resulted in proteins with slightly less stability, but which were nevertheless able to fold.

[0019] The positions of the internal breakpoints used in the studies cited here are found exclusively on the surface of proteins, and are distributed throughout the linear sequence without any obvious bias towards the ends or the middle (the variation in the relative distance from the original N-terminus to the breakpoint is ca. 10 to 80% of the total sequence length). The linkers connecting the original N- and C-termini in these studies have ranged from 0 to 9 residues. In one case (Yang & Schachman, *Proc. Natl. Acad. Sci. U.S.A.* **90**:11980-11984, 1993), a portion of sequence has been deleted from the original C-terminal segment, and the connection made from the truncated C-terminus to the original N-terminus. Flexible hydrophilic residues such as Gly and Ser are frequently used in the linkers. Viguera, et al.(*J. Mol. Biol.* **247**:670-681, 1995) compared joining the original N- and C-termini with 3- or 4-residue linkers; the 3-residue linker was less thermodynamically stable. Protasova et al. (*Protein Eng.* **7**:1373-1377, 1994) used 3- or 5-residue linkers in connecting the original N-termini of *E. coli* dihydrofolate reductase; only the 3-residue linker produced protein in good yield.

BRIEF SUMMARY OF THE INVENTION

[0020] Novel hematopoietic proteins of this invention are represented by the formulas:

R_1-L_1-R_2, R_2-L_1-R_1, R_1-R_2, or R_2-R_1

wherein R_1 and R_2 are independently selected from the group consisting of;

(I) A polypeptide comprising; a modified human G-CSF amino acid sequence of the formula:

```
1                                   10
Xaa Xaa Xaa Gly Pro Ala Ser Ser Leu Pro Gln Ser Xaa

                        20
Leu Leu Xaa Xaa Xaa Glu Gln Val Xaa Lys Xaa Gln Gly Xaa Gly

    30                                      40
Ala Xaa Leu Gln Glu Xaa Leu Xaa Ala Thr Tyr Lys Leu Xaa Xaa

                        50
Xaa Glu Xaa Xaa Val Xaa Xaa Gly His Ser Xaa Gly Ile Pro Trp

    60                                      70
Ala Pro Leu Ser Ser Xaa Pro Ser Xaa Ala Leu Xaa Leu Ala Gly

                        80
Xaa Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu

    90                                      100
Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu

                        110
Xaa Thr Leu Gln Xaa Asp Val Ala Asp Phe Ala Xaa Thr Ile Trp

    120                                     130
Gln Gln Met Glu Xaa Xaa Gly Met Ala Pro Ala Leu Gln Pro Thr

                        140
Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Xaa Gln Xaa Xaa Ala

    150                                     160
Gly Gly Val Leu Val Ala Ser Xaa Leu Gln Xaa Phe Leu Xaa Xaa

                        170
Ser Tyr Arg Val Leu Xaa Xaa Leu Ala Gln Pro  (SEQ ID NO:1)
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wherein

Xaa at position 1 is Thr, Ser, Arg, Tyr or Gly;
Xaa at position 2 is Pro or Leu;
Xaa at position 3 is Leu, Arg, Tyr or Ser;
Xaa at position 13 is Phe, Ser, His, Thr or Pro;
Xaa at position 16 is Lys, Pro, Ser, Thr or His;

Xaa at position 17 is Cys, Ser, Gly, Ala, Ile, Tyr or Arg;
Xaa at position 18 is Leu, Thr, Pro, His, Ile or Cys;
Xaa at position 22 is Arg, Tyr, Ser, Thr or Ala;
Xaa at position 24 is Ile, Pro, Tyr or Leu;
Xaa at position 27 is Asp, or Gly;
Xaa at position 30 is Ala, Ile, Leu or Gly;
Xaa at position 34 is Lys or Ser;
Xaa at position 36 is Cys or Ser;
Xaa at position 42 is Cys or Ser;
Xaa at position 43 is His, Thr, Gly, Val, Lys, Trp, Ala, Arg, Cys, or Leu;
Xaa at position 44 is Pro, Gly, Arg, Asp, Val, Ala, His, Trp, Gln, or Thr;
Xaa at position 46 is Glu, Arg, Phe, Arg, Ile or Ala;
Xaa at position 47 is Leu or Thr;
Xaa at position 49 is Leu, Phe, Arg or Ser;
Xaa at position 50 is Leu, Ile, His, Pro or Tyr;
Xaa at position 54 is Leu or His;
Xaa at position 64 is Cys or Ser;
Xaa at position 67 is Gln, Lys, Leu or Cys;
Xaa at position 70 is Gln, Pro, Leu, Arg or Ser;
Xaa at position 74 is Cys or Ser;
Xaa at position 104 is Asp, Gly or Val;
Xaa at position 108 is Leu, Ala, Val, Arg, Trp, Gln or Gly;
Xaa at position 115 is Thr, His, Leu or Ala;
Xaa at position 120 is Gln, Gly, Arg, Lys or His
Xaa at position 123 is Glu, Arg, Phe or Thr
Xaa at position 144 is Phe, His, Arg, Pro, Leu, Gln or Glu;
Xaa at position 146 is Arg or Gln;
Xaa at position 147 is Arg or Gln;
Xaa at position 156 is His, Gly or Ser;
Xaa at position 159 is Ser, Arg, Thr, Tyr, Val or Gly;
Xaa at position 162 is Glu, Leu, Gly or Trp;
Xaa at position 163 is Val, Gly, Arg or Ala;
Xaa at position 169 is Arg, Ser, Leu, Arg or Cys;
Xaa at position 170 is His, Arg or Ser;

wherein optionally 1-11 amino acids from the N-terminus and 1-5 from the C-terminus can be deleted; and

wherein the N-terminus is joined to the C-terminus directly or through a linker capable of joining the N-terminus to the C-

terminus and having new C- and N-termini at amino acids;

38-39	62-63	123-124
39-40	63-64	124-125
40-41	64-65	125-126
41-42	65-66	126-127
42-43	66-67	128-129
43-44	67-68	128-129
45-46	68-69	129-130
48-49	69-70	130-131
49-50	70-71	131-132
52-53	71-72	132-133
53-54	91-92	133-134
54-55	92-93	134-135
55-56	93-94	135-136
56-57	94-95	136-137
57-58	95-96	137-138
58-59	96-97	138-139
59-60	97-98	139-140
60-61	98-99	140-141
61-62	99-100	141-142
		or 142-143;

(II) A polypeptide comprising; a modified hIL-3 amino acid sequence of the formula:

Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp Val Asn
1 5 10 15

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50 55 60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65 70 75

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
80 85 90

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
95 100 105

Xaa Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
110 115 120

Xaa Xaa Xaa Gln Gln Thr Thr Leu Ser Leu Ala Ile Phe
125 130 (SEQ ID NO:2);

wherein

Xaa at position 17 is Ser, Lys, Gly, Asp, Met, Gln, or Arg;
Xaa at position 18 is Asn, His, Leu, Ile, Phe, Arg, or Gln;
Xaa at position 19 is Met, Phe, Ile, Arg, Gly, Ala, or Cys;
Xaa at position 20 is Ile, Cys, Gln, Glu, Arg, Pro, or Ala;
Xaa at position 21 is Asp, Phe, Lys, Arg, Ala, Gly, Glu, Gln, Asn, Thr, Ser or Val;
Xaa at position 22 is Glu, Trp, Pro, Ser, Ala, His, Asp, Asn, Gln, Leu, Val or Gly;
Xaa at position 23 is Ile, Val, Ala, Gly, Trp, Lys, Phe, Leu, Ser, or Arg;
Xaa at position 24 is Ile, Gly, Val, Arg, Ser, Phe, or Leu;
Xaa at position 25 is Thr, His, Gly, Gln, Arg, Pro, or Ala;
Xaa at position 26 is His, Thr, Phe, Gly, Arg, Ala, or Trp;
Xaa at position 27 is Leu, Gly, Arg, Thr, Ser, or Ala;

Xaa at position 28 is Lys, Arg, Leu, Gln, Gly, Pro, Val or Trp;
Xaa at position 29 is Gln, Asn, Leu, Pro, Arg, or Val;
Xaa at position 30 is Pro, His, Thr, Gly, Asp, Gln, Ser, Leu, or Lys;
Xaa at position 31 is Pro, Asp, Gly, Ala, Arg, Leu, or Gln;
Xaa at position 32 is Leu, Val, Arg, Gln, Asn, Gly, Ala, or Glu;
Xaa at position 33 is Pro, Leu, Gln, Ala, Thr, or Glu;
Xaa at position 34 is Leu, Val, Gly, Ser, Lys, Glu, Gln, Thr,Arg, Ala, Phe, Ile or Met;
Xaa at position 35 is Leu, Ala, Gly, Asn, Pro, Gln, or Val;
Xaa at position 36 is Asp, Leu, or Val;
Xaa at position 37 is Phe, Ser, Pro, Trp, or Ile;
Xaa at position 38 is Asn, or Ala;
Xaa at position 40 is Leu, Trp, or Arg;
Xaa at position 41 is Asn, Cys, Arg, Leu, His, Met, or Pro;
Xaa at position 42 is Gly, Asp, Ser, Cys, Asn, Lys, Thr, Leu, Val, Glu, Phe, Tyr, Ile, Met or Ala;
Xaa at position 43 is Glu, Asn, Tyr, Leu, Phe, Asp, Ala, Cys,Gln, Arg, Thr, Gly or Ser;
Xaa at position 44 is Asp, Ser, Leu, Arg, Lys, Thr, Met, Trp, Glu, Asn, Gln, Ala or Pro;
Xaa at position 45 is Gln, Pro, Phe, Val, Met, Leu, Thr, Lys, Trp, Asp, Asn, Arg, Ser, Ala, Ile, Glu or His;
Xaa at position 46 is Asp, Phe, Ser, Thr, Cys, Glu, Asn, Gln, Lys, His, Ala, Tyr, Ile, Val or Gly;
Xaa at position 47 is Ile, Gly, Val, Ser, Arg, Pro, or His;
Xaa at position 48 is Leu, Ser, Cys, Arg, Ile, His, Phe, Glu, Lys, Thr, Ala, Met, Val or Asn;
Xaa at position 49 is Met, Arg, Ala, Gly, Pro, Asn, His, or Asp;
Xaa at position 50 is Glu, Leu, Thr, Asp, Tyr, Lys, Asn, Ser, Ala, Ile, Val, His, Phe, Met or Gln;
Xaa at position 51 is Asn, Arg, Met, Pro, Ser, Thr, or His;
Xaa at position 52 is Asn, His, Arg, Leu, Gly, Ser, or Thr;
Xaa at position 53 is Leu, Thr, Ala, Gly, Glu, Pro, Lys, Ser, or Met;
Xaa at position 54 is Arg, Asp, Ile, Ser, Val, Thr, Gln, Asn, Lys, His, Ala or Leu;
Xaa at position 55 is Arg, Thr, Val, Ser, Leu, or Gly;
Xaa at position 56 is Pro, Gly, Cys, Ser, Gln, Glu, Arg, His, Thr, Ala, Tyr, Phe, Leu, Val or Lys;
Xaa at position 57 is Asn or Gly;
Xaa at position 58 is Leu, Ser, Asp, Arg, Gln, Val, or Cys;
Xaa at position 59 is Glu Tyr, His, Leu, Pro, or Arg;
Xaa at position 60 is Ala, Ser, Pro, Tyr, Asn, or Thr;

Xaa at position 61 is Phe, Asn, Glu, Pro, Lys, Arg, or Ser;
Xaa at position 62 is Asn, His, Val, Arg, Pro, Thr, Asp, or Ile;
Xaa at position 63 is Arg, Tyr, Trp, Lys, Ser, His, Pro, or Val;
Xaa at position 64 is Ala, Asn, Pro, Ser, or Lys;
Xaa at position 65 is Val, Thr, Pro, His, Leu, Phe, or Ser;
Xaa at position 66 is Lys, Ile, Arg, Val, Asn, Glu, or Ser;
Xaa at position 67 is Ser, Ala, Phe, Val, Gly, Asn, Ile, Pro, or His;
Xaa at position 68 is Leu, Val, Trp, Ser, Ile, Phe, Thr, or His;
Xaa at position 69 is Gln, Ala, Pro, Thr, Glu, Arg, Trp, Gly, or Leu;
Xaa at position 70 is Asn, Leu, Val, Trp, Pro, or Ala;
Xaa at position 71 is Ala, Met, Leu, Pro, Arg, Glu, Thr, Gln, Trp, or Asn;
Xaa at position 72 is Ser, Glu, Met, Ala, His, Asn, Arg, or Asp;
Xaa at position 73 is Ala, Glu, Asp, Leu, Ser, Gly, Thr, or Arg;
Xaa at position 74 is Ile, Met, Thr, Pro, Arg, Gly, Ala;
Xaa at position 75 is Glu, Lys, Gly, Asp, Pro, Trp, Arg, Ser, Gln, or Leu;
Xaa at position 76 is Ser, Val, Ala, Asn, Trp, Glu, Pro, Gly, or Asp;
Xaa at position 77 is Ile, Ser, Arg, Thr, or Leu;
Xaa at position 78 is Leu, Ala, Ser, Glu, Phe, Gly, or Arg;
Xaa at position 79 is Lys, Thr, Asn, Met, Arg, Ile, Gly, or Asp;
Xaa at position 80 is Asn, Trp, Val, Gly, Thr, Leu, Glu, or Arg;
Xaa at position 81 is Leu, Gln, Gly, Ala, Trp, Arg, Val, or Lys;
Xaa at position 82 is Leu, Gln, Lys, Trp, Arg, Asp, Glu, Asn, His, Thr, Ser, Ala, Tyr, Phe, Ile, Met or Val;
Xaa at position 83 is Pro, Ala, Thr, Trp, Arg, or Met;
Xaa at position 84 is Cys, Glu, Gly, Arg, Met, or Val;
Xaa at position 85 is Leu, Asn, Val, or Gln;
Xaa at position 86 is Pro, Cys, Arg, Ala, or Lys;
Xaa at position 87 is Leu, Ser, Trp, or Gly;
Xaa at position 88 is Ala, Lys, Arg, Val, or Trp;
Xaa at position 89 is Thr, Asp, Cys, Leu, Val, Glu, His, Asn, or Ser;
Xaa at position 90 is Ala, Pro, Ser, Thr, Gly, Asp, Ile, or Met;
Xaa at position 91 is Ala, Pro, Ser, Thr, Phe, Leu, Asp, or

His;
Xaa at position 92 is Pro, Phe, Arg, Ser, Lys, His, Ala, Gly, Ile or Leu;
Xaa at position 93 is Thr, Asp, Ser, Asn, Pro, Ala, Leu, or Arg;
Xaa at position 94 is Arg, Ile, Ser, Glu, Leu, Val, Gln, Lys, His, Ala, or Pro;
Xaa at position 95 is His, Gln, Pro, Arg, Val, Leu, Gly, Thr, Asn, Lys, Ser, Ala, Trp, Phe, Ile, or Tyr;
Xaa at position 96 is Pro, Lys, Tyr, Gly, Ile, or Thr;
Xaa at position 97 is Ile, Val, Lys, Ala, or Asn;
Xaa at position 98 is His, Ile, Asn, Leu, Asp, Ala, Thr, Glu, Gln, Ser, Phe, Met, Val, Lys, Arg, Tyr or Pro;
Xaa at position 99 is Ile, Leu, Arg, Asp, Val, Pro, Gln, Gly, Ser, Phe, or His;
Xaa at position 100 is Lys, Tyr, Leu, His, Arg, Ile, Ser, Gln, or Pro;
Xaa at position 101 is Asp, Pro, Met, Lys, His, Thr, Val, Tyr, Glu, Asn, Ser, Ala, Gly, Ile, Leu, or Gln;
Xaa at position 102 is Gly, Leu, Glu, Lys, Ser, Tyr, or Pro;
Xaa at position 103 is Asp, or Ser;
Xaa at position 104 is Trp, Val, Cys, Tyr, Thr, Met, Pro, Leu, Gln, Lys, Ala, Phe, or Gly;
Xaa at position 105 is Asn, Pro, Ala, Phe, Ser, Trp, Gln, Tyr, Leu, Lys, Ile, Asp, or His;
Xaa at position 106 is Glu, Ser, Ala, Lys, Thr, Ile, Gly, or Pro;
Xaa at position 108 is Arg, Lys, Asp, Leu, Thr, Ile, Gln, His, Ser, Ala or Pro;
Xaa at position 109 is Arg, Thr, Pro, Glu, Tyr, Leu, Ser, or Gly;
Xaa at position 110 is Lys, Ala, Asn, Thr, Leu, Arg, Gln, His, Glu, Ser, or Trp;
Xaa at position 111 is Leu, Ile, Arg, Asp, or Met;
Xaa at position 112 is Thr, Val, Gln, Tyr, Glu, His, Ser, or Phe;
Xaa at position 113 is Phe, Ser, Cys, His, Gly, Trp, Tyr, Asp, Lys, Leu, Ile, Val or Asn;
Xaa at position 114 is Tyr, Cys, His, Ser, Trp, Arg, or Leu;
Xaa at position 115 is Leu, Asn, Val, Pro, Arg, Ala, His, Thr, Trp, or Met;
Xaa at position 116 is Lys, Leu, Pro, Thr, Met, Asp, Val, Glu, Arg, Trp, Ser, Asn, His, Ala, Tyr, Phe, Gln, or Ile;
Xaa at position 117 is Thr, Ser, Asn, Ile, Trp, Lys, or Pro;
Xaa at position 118 is Leu, Ser, Pro, Ala, Glu, Cys, Asp, or Tyr;
Xaa at position 119 is Glu, Ser, Lys, Pro, Leu, Thr, Tyr, or

Arg;
Xaa at position 120 is Asn, Ala, Pro, Leu, His, Val, or Gln;
Xaa at position 121 is Ala, Ser, Ile, Asn, Pro, Lys, Asp, or Gly;
Xaa at position 122 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr, or Cys;
Xaa at position 123 is Ala, Met, Glu, His, Ser, Pro, Tyr, or Leu;

wherein optionally from 1 to 14 amino acids can be deleted from the N-terminus and/or from 1 to 15 amino acids can be deleted from the C-terminus; and wherein from 0 to 44 of the amino acids designated by Xaa are different from the corresponding amino acids of native (1-133) human interleukin-3; and

wherein the N-terminus is joined to the C-terminus directly or through a linker (L_2) capable of joining the N-terminus to the C-terminus and having new C- and N-termini at amino acids;

26-27	49-50	83-84
27-28	50-51	84-85
28-29	51-52	85-86
29-30	52-53	86-87
30-31	53-54	87-88
31-32	54-55	88-89
32-33	64-65	89-90
33-34	65-66	90-91
34-35	66-67	91-92
35-36	67-68	92-93
36-37	68-69	97-98
37-38	69-70	98-99
38-39	70-71	99-100
39-40	71-72	100-101
40-41	72-73	101-102
41-42	82-83	102-103
		or 103-104;

or

(III) A polypeptide comprising; a modified human c-mpl ligand amino acid sequence of the formula:

```
SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSer
1               5                  10                  15

HisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrPro
            20                  25                  30

ValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGlu
        40                  45                  50

ThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAla
    60                  65                  70

AlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGly
80                  85                  90

GlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnXaaXaaXaa
                100                 105                 110

XaaGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHis
            115                 120                 125

LeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysVal
        135                 140                 145

ArgArgAlaProProThrThrAlaValProSerArgThrSerLeuValLeuThrLeu
    155                 160                 165

AsnGluLeuProAsnArgThrSerGlyLeuLeuGluThrAsnPheThrAlaSerAla
175                 180                 185

ArgThrThrGlySerGlyLeuLeuLysTrpGlnGlnGlyPheArgAlaLysIlePro
                195                 200                 205

GlyLeuLeuAsnGlnThrSerArgSerLeuAspGlnIleProGlyTyrLeuAsnArg
210                 215                 220

IleHisGluLeuLeuAsnGlyThrArgGlyLeuPheProGlyProSerArgArgThr
        230                 235                 240

LeuGlyAlaProAspIleSerSerGlyThrSerAspThrGlySerLeuProProAsn
    250                 255                 260

LeuGlnProGlyTyrSerProSerProThrHisProProThrGlyGlnTyrThrLeu
```

270 275 280 285

PheProLeuProProThrLeuProThrProValValGlnLeuHisProLeuLeuPro
290 295 300

AspProSerAlaProThrProThrProThrSerProLeuLeuAsnThrSerTyrThr
305 310 315 320

HisSerGlnAsnLeuSerGlnGluGly (SEQ ID NO:3)
325 330 332
153

wherein;

Xaa at position 112 is deleted or Leu, Ala, Val, Ile, Pro, Phe, Trp, or Met;
Xaa at position 113 is deleted or Pro, Phe, Ala, Val, Leu, Ile, Trp, or Met;
Xaa at position 114 is deleted or Pro, Phe, Ala, Val, Leu, Ile, Trp, or Met;
Xaa at position 115 is deleted or Gln, Gly, Ser, Thr, Tyr, or Asn; and

wherein the N-terminus is joined to the C-terminus directly or through a linker (L_2) capable of joining the N-terminus to the C-terminus and having new C- and N-termini at amino acids;

26-27	51-52	108-109
27-28	52-53	109-110
28-29	53-54	110-111
29-30	54-55	111-112
30-31	55-56	112-113
32-33	56-57	113-114
33-34	57-58	114-115
34-35	58-59	115-116
36-37	59-60	116-117
37-38	78-79	117-118
38-39	79-80	118-119
40-41	80-81	119-120
41-42	81-82	120-121
42-43	82-83	121-122
43-44	83-84	122-123
44-45	84-85	123-124
46-47	85-86	124-125
47-48	86-87	125-126
48-49	87-88	126-127
50-51	88-89	or 127-128;

or

(IV) A polypeptide comprising; a modified hIL-3 amino acid sequence of the formula:

```
Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp Val Asn
1               5                  10                  15

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                20                  25                  30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa
                35                  40                  45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                50                  55                  60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                65                  70                  75

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                80                  85                  90

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                95                  100                 105

Xaa Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                110                 115                 120

Xaa Xaa Xaa Gln Gln Thr Thr Leu Ser Leu Ala Ile Phe
                125                 130 (SEQ ID NO:2)
```

wherein

Xaa at position 17 is Ser, Lys, Gly, Asp, Met, Gln, or Arg;
Xaa at position 18 is Asn, His, Leu, Ile, Phe, Arg, or Gln;
Xaa at position 19 is Met, Phe, Ile, Arg, Gly, Ala, or Cys;
Xaa at position 20 is Ile, Cys, Gln, Glu, Arg, Pro, or Ala;
Xaa at position 21 is Asp, Phe, Lys, Arg, Ala, Gly, Glu, Gln, Asn, Thr, Ser or Val;
Xaa at position 22 is Glu, Trp, Pro, Ser, Ala, His, Asp, Asn, Gln, Leu, Val or Gly;
Xaa at position 23 is Ile, Val, Ala, Gly, Trp, Lys, Phe, Leu, Ser, or Arg;
Xaa at position 24 is Ile, Gly, Val, Arg, Ser, Phe, or Leu;
Xaa at position 25 is Thr, His, Gly, Gln, Arg, Pro, or Ala;
Xaa at position 26 is His, Thr, Phe, Gly, Arg, Ala, or Trp;
Xaa at position 27 is Leu, Gly, Arg, Thr, Ser, or Ala;

Xaa at position 28 is Lys, Arg, Leu, Gln, Gly, Pro, Val or Trp;
Xaa at position 29 is Gln, Asn, Leu, Pro, Arg, or Val;
Xaa at position 30 is Pro, His, Thr, Gly, Asp, Gln, Ser, Leu, or Lys;
Xaa at position 31 is Pro, Asp, Gly, Ala, Arg, Leu, or Gln;
Xaa at position 32 is Leu, Val, Arg, Gln, Asn, Gly, Ala, or Glu;
Xaa at position 33 is Pro, Leu, Gln, Ala, Thr, or Glu;
Xaa at position 34 is Leu, Val, Gly, Ser, Lys, Glu, Gln, Thr, Arg, Ala, Phe, Ile or Met;
Xaa at position 35 is Leu, Ala, Gly, Asn, Pro, Gln, or Val;
Xaa at position 36 is Asp, Leu, or Val;
Xaa at position 37 is Phe, Ser, Pro, Trp, or Ile;
Xaa at position 38 is Asn, or Ala;
Xaa at position 40 is Leu, Trp, or Arg;
Xaa at position 41 is Asn, Cys, Arg, Leu, His, Met, or Pro;
Xaa at position 42 is Gly, Asp, Ser, Cys, Asn, Lys, Thr, Leu, Val, Glu, Phe, Tyr, Ile, Met or Ala;
Xaa at position 43 is Glu, Asn, Tyr, Leu, Phe, Asp, Ala, Cys, Gln, Arg, Thr, Gly or Ser;
Xaa at position 44 is Asp, Ser, Leu, Arg, Lys, Thr, Met, Trp, Glu, Asn, Gln, Ala or Pro;
Xaa at position 45 is Gln, Pro, Phe, Val, Met, Leu, Thr, Lys, Trp, Asp, Asn, Arg, Ser, Ala, Ile, Glu or His;
Xaa at position 46 is Asp, Phe, Ser, Thr, Cys, Glu, Asn, Gln, Lys, His, Ala, Tyr, Ile, Val or Gly;
Xaa at position 47 is Ile, Gly, Val, Ser, Arg, Pro, or His;
Xaa at position 48 is Leu, Ser, Cys, Arg, Ile, His, Phe, Glu, Lys, Thr, Ala, Met, Val or Asn;
Xaa at position 49 is Met, Arg, Ala, Gly, Pro, Asn, His, or Asp;
Xaa at position 50 is Glu, Leu, Thr, Asp, Tyr, Lys, Asn, Ser, Ala, Ile, Val, His, Phe, Met or Gln;
Xaa at position 51 is Asn, Arg, Met, Pro, Ser, Thr, or His;
Xaa at position 52 is Asn, His, Arg, Leu, Gly, Ser, or Thr;
Xaa at position 53 is Leu, Thr, Ala, Gly, Glu, Pro, Lys, Ser, or Met;
Xaa at position 54 is Arg, Asp, Ile, Ser, Val, Thr, Gln, Asn, Lys, His, Ala or Leu;
Xaa at position 55 is Arg, Thr, Val, Ser, Leu, or Gly;
Xaa at position 56 is Pro, Gly, Cys, Ser, Gln, Glu, Arg, His, Thr, Ala, Tyr, Phe, Leu, Val or Lys;
Xaa at position 57 is Asn or Gly;
Xaa at position 58 is Leu, Ser, Asp, Arg, Gln, Val, or Cys;
Xaa at position 59 is Glu Tyr, His, Leu, Pro, or Arg;
Xaa at position 60 is Ala, Ser, Pro, Tyr, Asn, or Thr;

Xaa at position 61 is Phe, Asn, Glu, Pro, Lys, Arg, or Ser;
Xaa at position 62 is Asn, His, Val, Arg, Pro, Thr, Asp, or Ile;
Xaa at position 63 is Arg, Tyr, Trp, Lys, Ser, His, Pro, or Val;
Xaa at position 64 is Ala, Asn, Pro, Ser, or Lys;
Xaa at position 65 is Val, Thr, Pro, His, Leu, Phe, or Ser;
Xaa at position 66 is Lys, Ile, Arg, Val, Asn, Glu, or Ser;
Xaa at position 67 is Ser, Ala, Phe, Val, Gly, Asn, Ile, Pro, or His;
Xaa at position 68 is Leu, Val, Trp, Ser, Ile, Phe, Thr, or His;
Xaa at position 69 is Gln, Ala, Pro, Thr, Glu, Arg, Trp, Gly, or Leu;
Xaa at position 70 is Asn, Leu, Val, Trp, Pro, or Ala;
Xaa at position 71 is Ala, Met, Leu, Pro, Arg, Glu, Thr, Gln, Trp, or Asn;
Xaa at position 72 is Ser, Glu, Met, Ala, His, Asn, Arg, or Asp;
Xaa at position 73 is Ala, Glu, Asp, Leu, Ser, Gly, Thr, or Arg;
Xaa at position 74 is Ile, Met, Thr, Pro, Arg, Gly, Ala;
Xaa at position 75 is Glu, Lys, Gly, Asp, Pro, Trp, Arg, Ser, Gln, or Leu;
Xaa at position 76 is Ser, Val, Ala, Asn, Trp, Glu, Pro, Gly, or Asp;
Xaa at position 77 is Ile, Ser, Arg, Thr, or Leu;
Xaa at position 78 is Leu, Ala, Ser, Glu, Phe, Gly, or Arg;
Xaa at position 79 is Lys, Thr, Asn, Met, Arg, Ile, Gly, or Asp;
Xaa at position 80 is Asn, Trp, Val, Gly, Thr, Leu, Glu, or Arg;
Xaa at position 81 is Leu, Gln, Gly, Ala, Trp, Arg, Val, or Lys;
Xaa at position 82 is Leu, Gln, Lys, Trp, Arg, Asp, Glu, Asn, His, Thr, Ser, Ala, Tyr, Phe, Ile, Met or Val;
Xaa at position 83 is Pro, Ala, Thr, Trp, Arg, or Met;
Xaa at position 84 is Cys, Glu, Gly, Arg, Met, or Val;
Xaa at position 85 is Leu, Asn, Val, or Gln;
Xaa at position 86 is Pro, Cys, Arg, Ala, or Lys;
Xaa at position 87 is Leu, Ser, Trp, or Gly;
Xaa at position 88 is Ala, Lys, Arg, Val, or Trp;
Xaa at position 89 is Thr, Asp, Cys, Leu, Val, Glu, His, Asn, or Ser;
Xaa at position 90 is Ala, Pro, Ser, Thr, Gly, Asp, Ile, or Met;
Xaa at position 91 is Ala, Pro, Ser, Thr, Phe, Leu, Asp, or

His;
Xaa at position 92 is Pro, Phe, Arg, Ser, Lys, His, Ala, Gly, Ile or Leu;
Xaa at position 93 is Thr, Asp, Ser, Asn, Pro, Ala, Leu, or Arg;
Xaa at position 94 is Arg, Ile, Ser, Glu, Leu, Val, Gln, Lys, His, Ala, or Pro;
Xaa at position 95 is His, Gln, Pro, Arg, Val, Leu, Gly, Thr, Asn, Lys, Ser, Ala, Trp, Phe, Ile, or Tyr;
Xaa at position 96 is Pro, Lys, Tyr, Gly, Ile, or Thr;
Xaa at position 97 is Ile, Val, Lys, Ala, or Asn;
Xaa at position 98 is His, Ile, Asn, Leu, Asp, Ala, Thr, Glu, Gln, Ser, Phe, Met, Val, Lys, Arg, Tyr or Pro;
Xaa at position 99 is Ile, Leu, Arg, Asp, Val, Pro, Gln, Gly, Ser, Phe, or His;
Xaa at position 100 is Lys, Tyr, Leu, His, Arg, Ile, Ser, Gln, or Pro;
Xaa at position 101 is Asp, Pro, Met, Lys, His, Thr, Val, Tyr, Glu, Asn, Ser, Ala, Gly, Ile, Leu, or Gln;
Xaa at position 102 is Gly, Leu, Glu, Lys, Ser, Tyr, or Pro;
Xaa at position 103 is Asp, or Ser;
Xaa at position 104 is Trp, Val, Cys, Tyr, Thr, Met, Pro, Leu, Gln, Lys, Ala, Phe, or Gly;
Xaa at position 105 is Asn, Pro, Ala, Phe, Ser, Trp, Gln, Tyr, Leu, Lys, Ile, Asp, or His;
Xaa at position 106 is Glu, Ser, Ala, Lys, Thr, Ile, Gly, or Pro;
Xaa at position 108 is Arg, Lys, Asp, Leu, Thr, Ile, Gln, His, Ser, Ala or Pro;
Xaa at position 109 is Arg, Thr, Pro, Glu, Tyr, Leu, Ser, or Gly;
Xaa at position 110 is Lys, Ala, Asn, Thr, Leu, Arg, Gln, His, Glu, Ser, or Trp;
Xaa at position 111 is Leu, Ile, Arg, Asp, or Met;
Xaa at position 112 is Thr, Val, Gln, Tyr, Glu, His, Ser, or Phe;
Xaa at position 113 is Phe, Ser, Cys, His, Gly, Trp, Tyr, Asp, Lys, Leu, Ile, Val or Asn;
Xaa at position 114 is Tyr, Cys, His, Ser, Trp, Arg, or Leu;
Xaa at position 115 is Leu, Asn, Val, Pro, Arg, Ala, His, Thr, Trp, or Met;
Xaa at position 116 is Lys, Leu, Pro, Thr, Met, Asp, Val, Glu, Arg, Trp, Ser, Asn, His, Ala, Tyr, Phe, Gln, or Ile;
Xaa at position 117 is Thr, Ser, Asn, Ile, Trp, Lys, or Pro;
Xaa at position 118 is Leu, Ser, Pro, Ala, Glu, Cys, Asp, or Tyr;
Xaa at position 119 is Glu, Ser, Lys, Pro, Leu, Thr, Tyr, or

Arg;
Xaa at position 120 is Asn, Ala, Pro, Leu, His, Val, or Gln;
Xaa at position 121 is Ala, Ser, Ile, Asn, Pro, Lys, Asp, or Gly;
Xaa at position 122 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr, or Cys;
Xaa at position 123 is Ala, Met, Glu, His, Ser, Pro, Tyr, or Leu;

wherein optionally from 1 to 14 amino acids can be deleted from the N-terminus and/or from 1 to 15 amino acids can be deleted from the C-terminus; and wherein from 1 to 44 of the amino acids designated by Xaa are different from the corresponding amino acids of native (1-133) human interleukin-3;

or

(V) a colony stimulating factor;

and wherein L_1 is a linker capable of linking R_1 to R_2;

with the proviso that at least R_1 or R_2 is selected from the polypeptide of formula (I) , (II), or (III); and

said hematopoietic protein can optionally be immediately preceded by (methionine^{-1}), (alanine^{-1}) or (methionine^{-2}, alanine^{-1}).

[0021] The more preferred breakpoints at which new C-terminus and N-terminus can be made in the polypeptide (I) above are; 38-39, 39-40, 40-41, 41-42, 48-49, 53-54, 54-55, 55-56, 56-57, 57-58, 58-59, 59-60, 60-61, 61-62, 62-63, 64-65, 65-66, 66-67, 67-68, 68-69, 69-70, 96-97, 125-126, 126-127, 127-128, 128-129, 129-130, 130-131, 131-132, 132-133, 133-134, 134-135, 135-136, 136-137, 137-138, 138-139, 139-140, 140-141 and 141-142.

[0022] The most preferred breakpoints at which new C-terminus and N-terminus can be made in the polypeptide (I) above are; 38-39, 48-49, 96-97, 125-126, 132-133 and 141-142.

[0023] The more preferred breakpoints at which new C-terminus and N-terminus can be made in the polypeptide (II) above are; 28-29, 29-30, 30-31, 31-32, 32-33, 33-34, 34-35, 35-36, 36-37, 37-38, 38-39, 39-40, 66-67, 67-68, 68-69, 69-70, 70-71, 84-85, 85-86, 86-87, 87-88, 88-89, 89-90, 90-91, 98-99, 99-100, 100-101 and 101-102.

[0024] The most preferred breakpoints at which new C-terminus and N-terminus can be made in the polypeptide (II) above are; 34-35, 69-70 and 90-91.

[0025] The more preferred breakpoints at which new C-terminus and N-terminus can be made in the polypeptide (III) above or the amino acid sequence of (SEQ ID NO:256) are; 80-81, 81-82, 82-83, 83-84, 84-85, 85-86, 86-87, 108-109, 109-110, 110-111, 111-112, 112-113, 113-114, 114-115, 115-116, 116-117, 117-118, 118-119, 119-120, 120-121, 121-122, 122-123, 123-124, 124-125, 125-126 and 126-127.

[0026] The most preferred breakpoints at which new C-terminus and N-terminus can be made in the polypeptide (III) above or the amino acid sequence of (SEQ ID NO:256) are; 81-82, 108-109, 115-116, 119-120, 122-123 and 125-126.

[0027] The invention is also intended to include multifunctional receptor agoinist which comprises a sequence rearranged c-mpl receptor agonist in which the cysteine at position 7 and/or 151 are substituted with another amino acid. Preferably, the substitution at position 7 and 151 is Ser, Ala, Gly, His, Asn, Asp, Thr, Phe or Thr. More preferably, the substitution at position 7 and 151 is Ser, Ala, Gly, His or Asn.

[0028] The multifunctional receptor agonist of the present invention can also be represented by the following formula:

$$(T^1)_a-(L^1)_b-X^1-(L)_c-X^2-(L^2)_d-(T^2)_e$$

$$X^1-(L)_c-X^2-(L)-Y^1-(L)_c-Y^2$$

in which:

X^1 is a peptide comprising an amino acid sequence corresponding to the sequence of residues n+1 through J of the original protein having amino acids residues numbered sequentially 1 through J with an amino terminus at residue 1;

L is an optional linker;

X^2 is a peptide comprising an amino acid sequence of residues 1 through n of the original protein;

Y^1 is a peptide comprising an amino acid sequence corresponding to the sequence of residues n=1 through K of the original protein having amino acids residues numbered sequentially 1 through K with an amino terminus at residue 1;

Y^2 is a peptide comprising an amino acid sequence of residues 1 through n of the original protein;

L^1 and L^2 are optional peptide spacers:

n is an integer ranging from 1 to J-1;

b, c, and d are each independently 0 or 1;

a and e are either 0 or 1, provided that both a and e cannot both be 0; and

T^1 and T^2 are proteins.

[0029] Additionally, the present invention relates to recombinant expression vectors comprising nucleotide sequences encoding the multi-functional hematopoietic receptor agonists, related microbial expression systems, and processes for making the multi-functional hematopoietic receptor agonists. The invention also relates to pharmaceutical compositions containing the multi-functional hematopoietic receptor agonists, and methods for using the multi-functional hematopoietic receptor agonists.

[0030] In addition to the use of the multi-functional hematopoietic receptor agonists of the present invention in vivo, it is envisioned that in vitro uses would include the ability to stimulate bone marrow and blood cell activation and growth before infusion into patients.

BRIEF DESCRIPTION OF THE FIGURES

[0031] Figure 1 schematically illustrates the sequence rearrangement of a protein. The N-terminus (N) and the C-terminus (C) of the native protein are joined through a linker, or joined directly. The protein is opened at a breakpoint creating a new N-terminus (new N) and a new C-terminus (new-C) resulting in a protein with a new linear amino acid sequence. A rearranged molecule may be synthesized *de novo* as linear molecule and not go through the steps of joining the original N-terminus and the C-terminus and opening of the protein at the breakpoint.

[0032] Figure 2 shows a schematic of Method I, for creating new proteins in which the original N-terminus and C-terminus of the native protein are joined with a linker and different N-terminus and C-terminus of the protein are created. In the example shown the sequence rearrangement results in a new gene encoding a protein with a new N-terminus created at amino acid 97 of the original protein, the original C-terminus (a.a. 174) joined to the amino acid 11 (a.a. 1- 10 are deleted) through a linker region and a new C-terminus created at amino acid 96 of the original sequence.

[0033] Figure 3 shows a schematic of Method II, for creating new proteins in which the original N-terminus and C-terminus of the native protein are joined without a linker and

different N-terminus and C-terminus of the protein are created. In the example shown the sequence rearrangement results in a new gene encoding a protein with a new N-terminus created at amino acid 97 of the original protein, the original C-terminus (a.a. 174) joined to the original N-terminus and a new C-terminus created at amino acid 96 of the original sequence.

[0034] Figure 4 shows a schematic of Method III, for creating new proteins in which the original N-terminus and C-terminus of the native protein are joined with a linker and different N-terminus and C-terminus of the protein are created. In the example shown the sequence rearrangement results in a new gene encoding a protein with a new N-terminus created at amino acid 97 of the original protein, the original C-terminus (a.a. 174) joined to amino acid 1 through a linker region and a new C-terminus created at amino acid 96 of the original sequence.

DETAILED DESCRIPTION OF THE INVENTION

[0035] The present invention encompasses multi-functional hematopoietic receptor agonists formed from covalently linked polypeptides, each of which may act through a different and specific cell receptor to initiate complementary biological activities. Hematopoiesis requires a complex series of cellular events in which stem cells generate continuously into large populations of maturing cells in all major lineages. There are currently at least 20 known regulators with hematopoietic proliferative activity. Most of these proliferative regulators can only stimulate one or another type of colony formation in vitro, the precise pattern of colony formation stimulated by each regulator is quite distinctive. No two regulators stimulate exactly the same pattern of colony formation, as evaluated by colony numbers or, more importantly, by the lineage and maturation pattern of the cells making up the developing colonies. Proliferative responses can most readily be analyzed in simplified in vitro culture systems. Three quite different parameters can be distinguished: alteration in colony size, alteration in colony numbers and cell lineage. Two or more factors may act on the progenitor cell, inducing the formation of larger number of progeny thereby increasing the colony size. Two or more factors may allow increased number of progenitor cells to

proliferate either because distinct subsets of progenitors cells exist that respond exclusively to one factor or because some progenitors require stimulation by two or more factors before being able to respond. Activation of additional receptors on a cell by the use of two or more factors is likely to enhance the mitotic signal because of coalescence of initially differing signal pathways into a common final pathway reaching the nucleus (Metcalf, *Nature* **339**:27, 1989). Other mechanisms could explain synergy. For example, if one signaling pathway is limited by an intermediate activation of an additional signaling pathway which is caused by a second factor, then this may result in a super additive response. In some cases, activation of one receptor type can induce an enhanced expression of other receptors (Metcalf, *Blood* **82**:3515-3523, 1993). Two or more factors may result in a different pattern of cell lineages than from a single factor. The use of multi-functional hematopoietic receptor agonists may have a potential clinical advantage resulting from a proliferative response that is not possible by any single factor.

[0036] The receptors of hematopoietic and other growth factors can be grouped into two distinct families of related proteins: (1) tyrosine kinase receptors, including those for epidermal growth factor, M-CSF (Sherr, *Blood* **75**:1, 1990) and

SCF (Yarden et al., *EMBO J.* **6**:3341, 1987): and (2) hematopoietic receptors, not containing a tyrosine kinase domain, but exhibiting obvious homology in their extracellular domain (Bazan, *PNAS USA* **87**:6934-6938, 1990). Included in this latter group are erythropoietin (EPO) (D'Andrea et al., *Cell* **57**:277, 1989), GM-CSF (Gearing et al., *EMBO J.* **8**:3667, 1989), IL-3 (Kitamura et al., *Cell* **66**:1165, **1**991), G-CSF (Fukunaga et al., *J. Bio. Chem.* **265**:14008-15, 1990), IL-4 (Harada et al., *PNAS USA* **87**:857, 1990), IL-5 (Takaki et al., *EMBO J.* **9**:4367, 1990), IL-6 (Yamasaki et al., *Science* **241**:825, 1988), IL-7 (Goodwin et al., *Cell* **60**:941-51, 1990), LIF (Gearing et al., *EMBO J.* **10**:2839, 1991) and IL-2 (Cosman et al., *Mol*-Immunol. **23**: 935-94, 1986). Most of the latter group of receptors exists in a high-affinity form as heterodimers. After ligand binding, the specific a-chains become associated with at least one other receptor chain (b-chain, g-chain). Many of these factors share a common receptor subunit. The a-chains for GM-CSF, IL-3 and IL-5 share the same b-chain (Kitamura et al., *Cell* **66**:1165, 1991), Takaki et al., *EMBO J.* **10**:2833-8, 1991) and receptor complexes for IL-6, LIF and IL-11 share a common b-chain (gp130) (Taga et al., *Cell* **58**:573-81, 1989; Gearing et al., *Science* **255**:1434-7, 1992). The receptor complexes of IL-2, IL-4, IL-7, IL-9 and IL-15 share a common g-chain (Kondo et al., *Science* **262**:1874, 1993; Russell et al., *Science* **266**:

1042-1045, 1993; Noguchi et al., *Science* **262**:1877, 1993; Giri et al., *EMBO J.* **13**:2822-2830, 1994).

[0037] The use of a multiply acting hematopoietic factor may also have a potential advantage by reducing the demands placed on factor-producing cells and their induction systems. If there are limitations in the ability of a cell to produce a factor, then by lowering the required concentrations of each of the factors, and using them in combination may usefully reduce demands on the factor-producing cells. The use of a multiply acting hematopoietic factor may lower the amount of the factors that would be needed, probably reducing the likelihood of adverse side-effects.

[0038] Novel compounds of this invention are represented by a formula selected from the group consisting of:

R_1-L_1-R_2, R_2-L_1-R_1, R_1-R_2, and R_2-R_1

[0039] Where R_1 and R_2 are as defined above.

[0040] R_2 is preferably a colony stimulating factor with a different but complementary activity than R_1. By complementary activity is meant activity which enhances or changes the response to another cell modulator. The R_1 polypeptide is joined either directly or through a linker segment to the R_2 polypeptide. The term "directly" defines multi-functional hematopoietic receptor agonists in which the

polypeptides are joined without a peptide linker. Thus L_1 represents a chemical bond or polypeptide segment to which both R_1 and R_2 are joined in frame, most commonly L_1 is a linear peptide to which R1 and R_2 are joined by amide bonds linking the carboxy terminus of R_1 to the amino terminus of L_1 and carboxy terminus of L_1 to the amino terminus of R_2. By "joined in frame" is meant that there is no translation termination or disruption between the reading frames of the DNA encoding R_1 and R_2.

[0041] A non-exclusive list of other growth factors, i.e. colony stimulating factors (CSFs), are cytokines, lymphokines, interleukins, or hematopoietic growth factors which can be joined to (I), (II) or (III) include GM-CSF, G-CSF, c-mpl ligand (also known as TPO or MGDF), M-CSF, erythropoietin (EPO), IL-1, IL-4, IL-2, IL-3, IL-5, IL 6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-15, LIF, flt3 ligand, human growth hormone, and stem cell factor (SCF) also known as steel factor or c-kit ligand. Additionally, this invention encompasses the use of modified R_1 or R_2 molecules or mutated or modified DNA sequences encoding these R_1 or R_2 molecules. The present invention also includes multi-functional hematopoietic receptor agonists in which R_1 or R_2 is an hIL-3 variant, c-mpl ligand variant, or G-CSF variant. A "hIL-3

variant" is defined as a hIL-3 molecule which has amino acid substitutions and/or portions of hIL-3 deleted as disclosed in WO 94/12638, WO 94/12639 and WO 95/00646, as well as other variants known in the art. A "c-mpl ligand variant" is defined an c-mpl ligand molecule which has amino acid substitutions and/or portions of c-mpl ligand deleted, disclosed in United States Application Serial Number 08/383,035 as well as other variants known in the art. A "G-CSF variant" is defined an G-CSF molecule which has amino acid substitutions and/or portions of G-CSF deleted, as disclosed herein, as well as other variants known in the art.

[0042] The linking group (L_1) is generally a polypeptide of between 1 and 500 amino acids in length. The linkers joining the two molecules are preferably designed to (1) allow the two molecules to fold and act independently of each other, (2) not have a propensity for developing an ordered secondary structure which could interfere with the functional domains of the two proteins, (3) have minimal hydrophobic characteristics which could interact with the functional protein domains and (4) provide steric separation of R_1 and R_2 such that R_1 and R_2 could interact simultaneously with their corresponding receptors on a single cell. Typically surface amino acids in flexible protein regions include Gly, Asn and Ser. Virtually any permutation of amino acid sequences containing Gly, Asn

and Ser would be expected to satisfy the above criteria for a linker sequence. Other neutral amino acids, such as Thr and Ala, may also be used in the linker sequence. Additional amino acids may also be included in the linkers due to the addition of unique restriction sites in the linker sequence to facilitate construction of the multi-functional hematopoietic receptor agonists.

[0043] Preferred L_1 linkers of the present invention include sequences selected from the group of formulas:

$(Gly^3Ser)^n$ (SEQ ID NO:4), $(Gly^4Ser)^n$ (SEQ ID NO:5), $(Gly^5Ser)^n$ (SEQ ID NO:6), $(Gly^nSer)^n$ (SEQ ID NO:7) or $(AlaGlySer)^n$ (SEQ ID NO:8).

[0044] One example of a highly-flexible linker is the glycine and serine-rich spacer region present within the pIII protein of the filamentous bacteriophages, e.g. bacteriophages M13 or fd (Schaller et al., *PNAS USA* **72**: 737-741, 1975). This region provides a long, flexible spacer region between two domains of the pIII surface protein. The spacer region consists of the amino acid sequence:

GlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGluGlyGlyGlySerGluGlyGlyGlySerGluGlyGlyGlySerGluGlyGlyGlySerGlyGlyGlySer (SEQ ID NO:9).

[0045] The present invention also includes linkers in which an endopeptidase recognition sequence is included. Such a cleavage site may be valuable to separate the individual

components of the multi-functional hematopoietic receptor agonist to determine if they are properly folded and active in vitro. Examples of various endopeptidases include, but are not limited to, plasmin, enterokinase, kallikrein, urokinase, tissue plasminogen activator, clostripain, chymosin, collagenase, Russell's viper venom protease, postproline cleavage enzyme, V8 protease, Thrombin and factor Xa.

[0046] Peptide linker segments from the hinge region of heavy chain immunoglobulins IgG, IgA, IgM, IgD or IgE provide an angular relationship between the attached polypeptides. Especially useful are those hinge regions where the cysteines are replaced with serines. Preferred linkers of the present invention include sequences derived from murine IgG gamma 2b hinge region in which the cysteines have been changed to serines. These linkers may also include an endopeptidase cleavage site. Examples of such linkers include the following sequences:

IleSerGluProSerGlyProIleSerThrIleAsnProSerProProSerLys
GluSerHisLysSerPro (SEQ ID NO:10) and

IleGluGlyArgIleSerGluProSerGlyProIleSerThrIleAsnProSer
ProProSerLysGluSerHisLysSerPro (SEQ ID NO:11).

[0047] The present invention is, however, not limited by the form, size or number of linker sequences employed and the only requirement of the linker is that functionally it does

not interfere with the folding and function of the individual molecules of the multi-functional hematopoietic receptor agonist.

[0048] One aspect of the invention includes multi-functional hematopoietic receptor agonists which comprise a sequence rearranged c-mpl receptor agonist in which the cysteine(s) at position 7 and 151 of c-mpl ligand, have been substituted with another amino acid. Kaushansky et al. (*Blood* **86**:255a Abstract 1008, 1995) teaches that all four of the cysteines at positions 7, 29, 85, and 151 are required for bioactivity. The presence of cysteines in a protein can cause problems in processing when the protein is being produced recombinantly in a bacterial host. Microbially produced cysteine-containing proteins may tend to form multimers which greatly complicate purification of the protein product. Several additional purification steps, such as reduction and reoxidation of the recombinant protein may be required to obtain the protein in the proper confirmation. Removal of one of the cysteine residues, with concurrent replacement by a chemically equivalent neutral amino acid, would be desirable, in order to simplify the isolation and purification of the molecule. However, the successful removal of cysteines from biologically active molecules is unpredictable, in that the tertiary structure in the absence of the normally formed

disulfide bridges, can be substantially altered. A molecule in which a pair of cysteines at positions 7 and 151 are substituted with another amino acid may have one or more advantages including, but not limited to: 1) increased folding efficiency of the heterologously expressed protein; 2) elimination of mispaired disulfides, 3) use of milder refold conditions (ie. Guanidine vs. Urea); 4) increased purification yields, 5) increased protein solubility; and 6) increased protein stability.

Determination of the Linker L_2.

[0049] The length of the amino acid sequence of the linker L_2 to be used in R_1 and/or R_2 can be selected empirically or with guidance from structural information, or by using a combination of the two approaches.

[0050] When no structural information is available, a small series of linkers can be prepared for testing using a design whose length is varied in order to span a range from 0 to 50 Å and whose sequence is chosen in order to be consistent with surface exposure (hydrophilicity, Hopp & Woods, *Mol. Immunol.* **20**: 483-489, 1983), Kyte & Doolittle, *J. Mol. Biol.* **157**:105-132; solvent exposed surface area, Lee & Richards, *J. Mol. Biol.* **55**:379-400, 1971) and the ability to adopt the necessary conformation with out deranging the conformation of R^1 or R^2

(conformationally flexible; Karplus & Schulz, *Naturwissenschaften* **72**:212-213, 1985). Assuming an average of translation of 2.0 to 3.8 Å per residue, this would mean the length to test would be between 0 to 30 residues, with 0 to 15 residues being the preferred range. Exemplary of such an empirical series would be to construct linkers using a cassette sequence such as Gly-Gly-Gly-Ser (SEQ ID NO:12) repeated n times, where n is 1, 2, 3 or 4. Those skilled in the art will recognize that there are many such sequences that vary in length or composition that can serve as linkers with the primary consideration being that they be neither excessively long nor short (cf., Sandhu, *Critical Rev. Biotech.* **12**: 437-462, 1992); if they are too long, entropy effects will likely destabilize the three-dimensional fold, and may also make folding kinetically impractical, and if they are too short, they will likely destabilize the molecule because of torsional or steric strain.

[0051] Those skilled in the analysis of protein structural information will recognize that using the distance between the chain ends, defined as the distance between the c-alpha carbons, can be used to define the length of the sequence to be used, or at least to limit the number of possibilities that must be tested in an empirical selection of linkers. They will also recognize that it is sometimes the case that the

positions of the ends of the polypeptide chain are ill-defined in structural models derived from x-ray diffraction or nuclear magnetic resonance spectroscopy data, and that when true, this situation will therefore need to be taken into account in order to properly estimate the length of the linker required. From those residues whose positions are well defined are selected two residues that are close in sequence to the chain ends, and the distance between their c-alpha carbons is used to calculate an approximate length for a linker between them. Using the calculated length as a guide, linkers with a range of number of residues (calculated using 2 to 3.8Å per residue) are then selected. These linkers may be composed of the original sequence, shortened or lengthened as necessary, and when lengthened the additional residues may be chosen to be flexible and hydrophilic as described above; or optionally the original sequence may be substituted for using a series of linkers, one example being the Gly-Gly-Gly-Ser (SEQ ID NO:12) cassette approach mentioned above; or optionally a combination of the original sequence and new sequence having the appropriate total length may be used.

Determination of the Amino and Carboxyl Termini of R_1 and R_2

[0052] Sequences of R_1 and R_2 capable of folding to biologically active states can be prepared by appropriate

selection of the beginning (amino terminus) and ending (carboxyl terminus) positions from within the original polypeptide chain while using the linker sequence L_2 as described above. Amino and carboxyl termini are selected from within a common stretch of sequence, referred to as a breakpoint region, using the guidelines described below. A novel amino acid sequence is thus generated by selecting amino and carboxyl termini from within the same breakpoint region. In many cases the selection of the new termini will be such that the original position of the carboxyl terminus immediately preceded that of the amino terminus. However, those skilled in the art will recognize that selections of termini anywhere within the region may function, and that these will effectively lead to either deletions or additions to the amino or carboxyl portions of the new sequence.

[0053] It is a central tenet of molecular biology that the primary amino acid sequence of a protein dictates folding to the three-dimensional structure necessary for expression of its biological function. Methods are known to those skilled in the art to obtain and interpret three-dimensional structural information using x-ray diffraction of single protein crystals or nuclear magnetic resonance spectroscopy of protein solutions. Examples of structural information that are relevant to the identification of breakpoint regions

include the location and type of protein secondary structure (alpha and 3-10 helices, parallel and anti-parallel beta sheets, chain reversals and turns, and loops; Kabsch & Sander, *Biopolymers* **22**: 2577-2637, 1983), the degree of solvent exposure of amino acid residues, the extent and type of interactions of residues with one another (Chothia, *Ann. Rev. Biochem.* **53**:537-572, 1984) and the static and dynamic distribution of conformations along the polypeptide chain (Alber & Mathews, *Methods Enzymol.* **154**: 511-533, 1987). In some cases additional information is known about solvent exposure of residues; one example is a site of post-translational attachment of carbohydrate which is necessarily on the surface of the protein. When experimental structural information is not available, or is not feasible to obtain, methods are also available to analyze the primary amino acid sequence in order to make predictions of protein tertiary and secondary structure, solvent accessibility and the occurrence of turns and loops. Biochemical methods are also sometimes applicable for empirically determining surface exposure when direct structural methods are not feasible; for example, using the identification of sites of chain scission following limited proteolysis in order to infer surface exposure (Gentile & Salvatore, *Eur. J. Biochem.* **218**:603-621, 1993)

[0054] Thus using either the experimentally derived structural information or predictive methods (e.g., Srinivisan & Rose *Proteins: Struct., Funct. & Genetics*, **22**: 81-99, 1995) the parental amino acid sequence is inspected to classify regions according to whether or not they are integral to the maintenance of secondary and tertiary structure. The occurrence of sequences within regions that are known to be involved in periodic secondary structure (alpha and 3-10 helices, parallel and anti-parallel beta sheets) are regions that should be avoided. Similarly, regions of amino acid sequence that are observed or predicted to have a low degree of solvent exposure are more likely to be part of the so-called hydrophobic core of the protein and should also be avoided for selection of amino and carboxyl termini. In contrast, those regions that are known or predicted to be in surface turns or loops, and especially those regions that are known not to be required for biological activity, are the preferred sites for location of the extremes of the polypeptide chain. Continuous stretches of amino acid sequence that are preferred based on the above criteria are referred to as a breakpoint region.

Non-covalent Multifunctional
Hematopoietic Growth Factors

[0055] An alternative method for connecting two hematopoietic growth factors is by means of a non-covalent interaction. Such complexed proteins can be described by one of the formulae:

R_1-C_1 + R_2-C_2; or C_1-R_1 + C_2-R_2; C_1-R_1 + R_2-C_2; or C_1-R_1 + R_2-C_2.

[0056] R_1 and R_2 are as is defined above. Domains C_1 and C_2 are either identical or non-identical chemical structures, typically proteinaceous, which can form a non-covalent, specific association. Complexes between C_1 and C_2 result in a one-to-one stoichiometric relationship between R_1 and R_2 for each complex. Examples of domains which associate are "leucine zipper" domains of transcription factors, dimerization domains of bacterial transcription repressors and immunoglobulin constant domains. Covalent bonds link R_1 and C_1, and R_2 and C_2, respectively. As indicated in the formulae, the domains C_1 and C_2 can be present either at the N-terminus or C-terminus of their corresponding hematopoietic growth factor (R). These multimerization domains (C_1 and C_2) include those derived from the bZIP family of proteins (Abel et al., Nature **341**:24-25, 1989; Landshulz et al., *Science* **240**:1759-1764, 1988; Pu et al., *Nuc. Acid Res.* **21**:4348-4355, 1993; Kozarides et al., *Nature* **336**:646-651, 1988), as well as multimerization domains of the helix-loop-helix family of

proteins (Abel et al., Nature **341**:24-25, 1989; Murre et al., *Cell* **56**:777-783, 1989; Tapscott et al., *Science* **242**:405-411, 1988; Fisher et al., *Genes & Dev.* **5**:2342-2352, 1991). Preferred multi-functional hematopoietic receptor agonists of the present invention include colony stimulating factors dimerized by virtue of their incorporation as translational multi-functional hematopoietic receptor agonists with the leucine zipper dimerization domains of the bZIP family proteins Fos and Jun. The leucine zipper domain of Jun is capable of interacting with identical domains. On the other hand, the leucine zipper domain of Fos interacts with the Jun leucine zipper domain, but does not interact with other Fos leucine zipper domains. Mixtures of Fos and Jun predominantly result in formation of Fos-Jun heterodimers. Consequently, when joined to colony stimulating factors, the Jun domain can be used to direct the formation of either homo- or heterodimers. Preferential formation of heterodimers can be achieved if one of the colony stimulating factor partners is engineered to possess the Jun leucine zipper domain while the other is engineered to possess the Fos zipper.

[0057] Additional peptide sequences may also be added to facilitate purification or identification of multi-functional hematopoietic receptor agonist proteins (e.g., poly-His). A highly antigenic peptide may also be added that would enable

rapid assay and facile purification of the multi-functional hematopoietic receptor agonist protein by a specific monoclonal antibody.

[0058] "Mutant amino acid sequence," "mutant protein", "variant protein", "mutein", or "mutant polypeptide" refers to a polypeptide having an amino acid sequence which varies from a native sequence due to amino acid deletions, substitutions, or both, or is encoded by a nucleotide sequence intentionally made variant from a native sequence.. "Native sequence" refers to an amino acid or nucleic acid sequence which is identical to a wild-type or native form of a gene or protein.

[0059] Hematopoietic growth factors can be characterized by their ability to stimulate colony formation by human hematopoietic progenitor cells. The colonies formed include erythroid, granulocyte, megakaryocyte, granulocytic macrophages and mixtures thereof. Many of the hematopoietic growth factors have demonstrated the ability to restore bone marrow function and peripheral blood cell populations to therapeutically beneficial levels in studies performed initially in primates and subsequently in humans. Many or all of these biological activities of hematopoietic growth factors involve signal transduction and high affinity receptor binding. Multi-functional hematopoietic receptor agonists of the present invention may exhibit useful properties such as

having similar or greater biological activity when compared to a single factor or by having improved half-life or decreased adverse side effects, or a combination of these properties.

[0060] Multi-functional hematopoietic receptor agonists which have little or no agonist activity maybe useful as antagonists, as antigens for the production of antibodies for use in immunology or immunotherapy, as genetic probes or as intermediates used to construct other useful hIL-3 muteins.

[0061] Biological activity of the multi-functional hematopoietic receptor agonist proteins of the present invention can be determined by DNA synthesis in factor-dependent cell lines or by counting the colony forming units in an in vitro bone marrow assay.

[0062] The multi-functional hematopoietic receptor agonists of the present invention may have an improved therapeutic profile as compared to single acting hematopoietic agonists. For example, some multi-functional hematopoietic receptor agonists of the present invention may have a similar or more potent growth factor activity relative to other hematopoietic agonists without having a similar or corresponding increase in side-effects.

[0063] The present invention also includes the DNA sequences which code for the multi-functional hematopoietic receptor agonist proteins, DNA sequences which are

substantially similar and perform substantially the same function, and DNA sequences which differ from the DNAs encoding the multi-functional hematopoietic receptor agonists of the invention only due to the degeneracy of the genetic code. Also included in the present invention are the oligonucleotide intermediates used to construct the mutant DNAs and the polypeptides coded for by these oligonucleotides.

[0064] Genetic engineering techniques now standard in the art (United States Patent 4,935,233 and Sambrook et al., "Molecular Cloning A Laboratory Manual", Cold Spring Harbor Laboratory, 1989) may be used in the construction of the DNA sequences of the present invention. One such method is cassette mutagenesis (Wells et al., *Gene* **34**:315-323, 1985) in which a portion of the coding sequence in a plasmid is replaced with synthetic oligonucleotides that encode the desired amino acid substitutions in a portion of the gene between two restriction sites.

[0065] Pairs of complementary synthetic oligonucleotides encoding the desired gene can be made and annealed to each other. The DNA sequence of the oligonucleotide would encode sequence for amino acids of desired gene with the exception of those substituted and/or deleted from the sequence.

[0066] Plasmid DNA can be treated with the chosen restriction endonucleases then ligated to the annealed

oligonucleotides. The ligated mixtures can be used to transform competent JM101 cells to resistance to an appropriate antibiotic. Single colonies can be picked and the plasmid DNA examined by restriction analysis and/or DNA sequencing to identify plasmids with the desired genes.

[0067] Cloning of the DNA sequences of the novel multifunctional hematopoietic agonists wherein at least one of the with the DNA sequence of the other colony stimulating factor may be accomplished by the use of intermediate vectors. Alternatively one gene can be cloned directly into a vector containing the other gene. Linkers and adapters can be used for joining the DNA sequences, as well as replacing lost sequences, where a restriction site was internal to the region of interest. Thus genetic material (DNA) encoding one polypeptide, peptide linker, and the other polypeptide is inserted into a suitable expression vector which is used to transform bacteria, yeast, insect cells or mammalian cells. The transformed organism is grown and the protein isolated by standard techniques. The resulting product is therefore a new protein which has a colony stimulating factor joined by a linker region to a second colony stimulating factor.

[0068] Another aspect of the present invention provides plasmid DNA vectors for use in the expression of these novel multi-functional hematopoietic receptor agonists. These

vectors contain the novel DNA sequences described above which code for the novel polypeptides of the invention. Appropriate vectors which can transform microorganisms capable of expressing the multi-functional hematopoietic receptor agonists include expression vectors comprising nucleotide sequences coding for the multi-functional hematopoietic receptor agonists joined to transcriptional and translational regulatory sequences which are selected according to the host cells used.

[0069] Vectors incorporating modified sequences as described above are included in the present invention and are useful in the production of the multi-functional hematopoietic receptor agonist polypeptides. The vector employed in the method also contains selected regulatory sequences in operative association with the DNA coding sequences of the invention and which are capable of directing the replication and expression thereof in selected host cells.

[0070] As another aspect of the present invention, there is provided a method for producing the novel multi-functional hematopoietic receptor agonists. The method of the present invention involves culturing suitable cells or cell line, which has been transformed with a vector containing a DNA sequence coding for expression of a novel multi-functional hematopoietic receptor agonist. Suitable cells or cell lines

may be bacterial cells. For example, the various strains of *E. coli* are well-known as host cells in the field of biotechnology. Examples of such strains include *E. coli* strains JM101 (Yanish-Perron et al. *Gene* **33**: 103-119, 1985) and MON105 (Obukowicz et al., *Applied Environmental Microbiology* **58**: 1511-1523, 1992). Also included in the present invention is the expression of the multi-functional hematopoietic receptor agonist protein utilizing a chromosomal expression vector for *E. coli* based on the bacteriophage Mu (Weinberg et al., *Gene* **126**: 25-33, 1993). Various strains of *B. subtilis* may also be employed in this method. Many strains of yeast cells known to those skilled in the art are also available as host cells for expression of the polypeptides of the present invention. When expressed in the *E. coli* cytoplasm, the gene encoding the multi-functional hematopoietic receptor agonists of the present invention may also be constructed such that at the 5′ end of the gene codons are added to encode Met^{-2}-Ala^{-1}- or Met^{-1} at the N-terminus of the protein. The N termini of proteins made in the cytoplasm of *E. coli* are affected by post-translational processing by methionine aminopeptidase (Ben Bassat et al., *J. Bac.* **169**:751-757, 1987) and possibly by other peptidases so that upon expression the methionine is cleaved off the N-terminus. The multi-functional hematopoietic receptor agonists of the

present invention may include multi-functional hematopoietic receptor agonist polypeptides having Met^{-1}, Ala^{-1} or Met^{-2}-Ala^{-1} at the N-terminus. These mutant multi-functional hematopoietic receptor agonists may also be expressed in *E. coli* by fusing a secretion signal peptide to the N-terminus. This signal peptide is cleaved from the polypeptide as part of the secretion process.

[0071] Also suitable for use in the present invention are mammalian cells, such as Chinese hamster ovary cells (CHO). General methods for expression of foreign genes in mammalian cells are reviewed in Kaufman, R. J., 1987) Genetic Engineering, Principles and Methods, Vol. 9, J. K. Setlow, editor, Plenum Press, New York. An expression vector is constructed in which a strong promoter capable of functioning in mammalian cells drives transcription of a eukaryotic secretion signal peptide coding region, which is translationally joined to the coding region for the multi-functional hematopoietic receptor agonist. For example, plasmids such as pcDNA I/Neo, pRc/RSV, and pRc/CMV (obtained from Invitrogen Corp., San Diego, California) can be used. The eukaryotic secretion signal peptide coding region can be from the gene itself or it can be from another secreted mammalian protein (Bayne, M. L. et al., *Proc. Natl. Acad. Sci.*

USA **84**: 2638-2642, 1987). After construction of the vector containing the gene, the vector DNA is transfected into mammalian cells. Such cells can be, for example, the COS7, HeLa, BHK, CHO, or mouse L lines. The cells can be cultured, for example, in DMEM media (JRH Scientific). The polypeptide secreted into the media can be recovered by standard biochemical approaches following transient expression for 24 - 72 hours after transfection of the cells or after establishment of stable cell lines following selection for antibiotic resistance. The selection of suitable mammalian host cells and methods for transformation, culture, amplification, screening and product production and purification are known in the art. See, e.g., Gething and Sambrook, *Nature*, **293**:620-625, 1981), or alternatively, Kaufman et al, *Mol. Cell. Biol.*, **5(7)**:1750-1759, 1985) or Howley et al., U.S. Pat. No. 4,419,446. Another suitable mammalian cell line is the monkey COS-1 cell line. A similarly useful mammalian cell line is the CV-1 cell line.

[0072] Where desired, insect cells may be utilized as host cells in the method of the present invention. See, e.g., Miller et al., *Genetic Engineering*, **8**:277-298 (Plenum Press 1986) and references cited therein. In addition, general methods for expression of foreign genes in insect cells using Baculovirus vectors are described in: Summers, M. D. and

Smith, G. E., 1987) - A manual of methods for Baculovirus vectors and insect cell culture procedures, Texas Agricultural Experiment Station Bulletin No. 1555. An expression vector is constructed comprising a Baculovirus transfer vector, in which a strong Baculovirus promoter (such as the polyhedron promoter) drives transcription of a eukaryotic secretion signal peptide coding region, which is translationally joined to the coding region for the multi-functional hematopoietic receptor agonist polypeptide. For example, the plasmid pVL1392 (obtained from Invitrogen Corp., San Diego, California) can be used. After construction of the vector carrying the gene encoding the multi-functional hematopoietic receptor agonist polypeptide, two micrograms of this DNA is co-transfected with one microgram of Baculovirus DNA (see Summers & Smith, 1987) into insect cells, strain SF9. Pure recombinant Baculovirus carrying the multi-functional hematopoietic receptor agonist is used to infect cells cultured, for example, in Excell 401 serum-free medium (JRH Biosciences, Lenexa, Kansas). The multi-functional hematopoietic receptor agonist secreted into the medium can be recovered by standard biochemical approaches. Supernatants from mammalian or insect cells expressing the multi-functional hematopoietic receptor agonist protein can be first

concentrated using any of a number of commercial concentration units.

[0073] The multi-functional hematopoietic receptor agonists of the present invention may be useful in the treatment of diseases characterized by decreased levels of either myeloid, erythroid, lymphoid, or megakaryocyte cells of the hematopoietic system or combinations thereof. In addition, they may be used to activate mature myeloid and/or lymphoid cells. Among conditions susceptible to treatment with the polypeptides of the present invention is leukopenia, a reduction in the number of circulating leukocytes (white cells) in the peripheral blood. Leukopenia may be induced by exposure to certain viruses or to radiation. It is often a side effect of various forms of cancer therapy, e.g., exposure to chemotherapeutic drugs, radiation and of infection or hemorrhage. Therapeutic treatment of leukopenia with these multi-functional hematopoietic receptor agonists of the present invention may avoid undesirable side effects caused by treatment with presently available drugs.

[0074] The multi-functional hematopoietic receptor agonists of the present invention may be useful in the treatment of neutropenia and, for example, in the treatment of such conditions as aplastic anemia, cyclic neutropenia, idiopathic neutropenia, Chediak-Higashi syndrome, systemic lupus

erythematosus (SLE), leukemia, myelodysplastic syndrome and myelofibrosis.

[0075] The multi-functional hematopoietic receptor agonist of the present invention may be useful in the treatment or prevention of thrombocytopenia. Currently the only therapy for thrombocytopenia is platelet transfusion which are costly and carry the significant risks of infection (HIV, HBV) and alloimmunization. The multi-functional hematopoietic receptor agonist may alleviate or diminish the need for platelet transfusion. Severe thrombocytopenia may result from genetic defects such as Fanconi's Anemia, Wiscott-Aldrich, or May Hegglin syndromes. Acquired thrombocytopenia may result from auto- or allo-antibodies as in Immune Thrombocytopenia Purpura, Systemic Lupus Erythromatosis, hemolytic anemia, or fetal maternal incompatibility. In addition, splenomegaly, disseminated intravascular coagulation, thrombotic thrombocytopenic purpura, infection or prosthetic heart valves may result in thrombocytopenia. Severe thrombocytopenia may also result from chemotherapy and/or radiation therapy or cancer. Thrombocytopenia may also result from marrow invasion by carcinoma, lymphoma, leukemia or fibrosis.

[0076] The multi-functional hematopoietic receptor agonists of the present invention may be useful in the mobilization of hematopoietic progenitors and stem cells in peripheral blood.

Peripheral blood derived progenitors have been shown to be effective in reconstituting patients in the setting of autologous marrow transplantation. Hematopoietic growth factors including G-CSF and GM-CSF have been shown to enhance the number of circulating progenitors and stem cells in the peripheral blood. This has simplified the procedure for peripheral stem cell collection and dramatically decreased the cost of the procedure by decreasing the number of pheresis required. The multi-functional hematopoietic receptor agonist may be useful in mobilization of stem cells and further enhance the efficacy of peripheral stem cell transplantation.

[0077] The multi-functional hematopoietic receptor agonists of the present invention may also be useful in the ex vivo expansion of hematopoietic progenitors and stem cells. Colony stimulating factors (CSFs), such as hIL-3, have been administered alone, co-administered with other CSFs, or in combination with bone marrow transplants subsequent to high dose chemotherapy to treat the neutropenia and thrombocytopenia which are often the result of such treatment. However the period of severe neutropenia and thrombocytopenia may not be totally eliminated. The myeloid lineage, which is comprised of monocytes (macrophages), granulocytes (including neutrophils) and megakaryocytes, is critical in preventing infections and bleeding which can be life-threatening.

Neutropenia and thrombocytopenia may also be the result of disease, genetic disorders, drugs, toxins, radiation and many therapeutic treatments such as conventional oncology therapy.

[0078] Bone marrow transplants have been used to treat this patient population. However, several problems are associated with the use of bone marrow to reconstitute a compromised hematopoietic system including: 1) the number of stem cells in bone marrow, spleen, or peripheral blood is limited, 2) Graft Versus Host Disease, 3) graft rejection and 4) possible contamination with tumor cells. Stem cells make up a very small percentage of the nucleated cells in the bone marrow, spleen and peripheral blood. It is clear that a dose response exists such that a greater number of stem cells will enhance hematopoietic recovery. Therefore, the in vitro expansion of stem cells should enhance hematopoietic recovery and patient survival. Bone marrow from an allogeneic donor has been used to provide bone marrow for transplant. However, Graft Versus Host Disease and graft rejection limit bone marrow transplantation even in recipients with HLA-matched sibling donors. An alternative to allogeneic bone marrow transplants is autologous bone marrow transplants. In autologous bone marrow transplants, some of the patient's own marrow is harvested prior to myeloablative therapy, e.g. high dose chemotherapy, and is transplanted back into the patient

afterwards. Autologous transplants eliminate the risk of Graft Versus Host Disease and graft rejection. However, autologous bone marrow transplants still present problems in terms of the limited number of stems cells in the marrow and possible contamination with tumor cells. The limited number of stem cells may be overcome by ex-vivo expansion of the stem cells. In addition, stem cells can be specifically isolated, based on the presence of specific surface antigens such as CD34+ in order to decrease tumor cell contamination of the marrow graft.

[0079] The following patents contain further details on separating stem cells, CD34+ cells, culturing the cells with hematopoietic factors, the use of the cells for the treatment of patients with hematopoietic disorders and the use of hematopoietic factors for cell expansion and gene therapy.

5,061,620 relates to compositions comprising human hematopoietic stem cells provided by separating the stem cells from dedicated cells.

5,199,942 describes a method for autologous hematopoietic cell transplantation comprising: (1) obtaining hematopoietic progenitor cells from a patient; (2) ex-vivo expansion of cells with a growth factor selected from the group consisting of IL-3, flt3 ligand, c-kit ligand, GM-CSF, IL-1, GM-CSF/IL-3 fusion protein and combinations thereof; (3) administering

cellular preparation to a patient.

5,240,856 relates to a cell separator that includes an apparatus for automatically controlling the cell separation process.

WO 91/16116 describes devices and methods for selectively isolating and separating target cells from a mixture of cells.

WO 91/18972 describes methods for in vitro culturing of bone marrow, by incubating suspension of bone marrow cells, using a hollow fiber bioreactor.

WO 92/18615 relates to a process for maintaining and expanding bone marrow cells, in a culture medium containing specific mixtures of cytokines, for use in transplants.

WO 93/08268 describes a method for selectively expanding stem cells, comprising the steps of (a) separating CD34+ stem cells from other cells and (b) incubating the separated cells in a selective medium, such that the stem cells are selectively expanded.

WO 93/18136 describes a process for in vitro support of mammalian cells derived from peripheral blood.

WO 93/18648 relates to a composition comprising human neutrophil precursor cells with a high content of myeloblasts and promyelocytes for treating genetic or acquired neutropenia.

WO 94/08039 describes a method of enrichment for human

hematopoietic stem cells by selection for cells which express c-kit protein.

WO 94/11493 describes a stem cell population that are CD34+ and small in size, which are isolated using a counterflow elutriation method.

WO 94/27698 relates to a method combining immunoaffinity separation and continuous flow centrifugal separation for the selective separation of a nucleated heterogeneous cell population from a heterogeneous cell mixture.

WO 94/25848 describes a cell separation apparatus for collection and manipulation of target cells.

[0080] The long term culturing of highly enriched CD34+ precursors of hematopoietic progenitor cells from human bone marrow in cultures containing IL-1a, IL-3, IL-6 or GM-CSF is discussed in Brandt et al *J. Clin. Invest.* **86**:932-941, 1990).

[0081] One aspect of the present invention provides a method for selective ex-vivo expansion of stem cells. The term "stem cell" refers to the totipotent hematopoietic stem cells as well as early precursors and progenitor cells which can be isolated from bone marrow, spleen or peripheral blood. The term "expansion" refers to the differentiation and proliferation of the cells. The present invention provides a method for selective ex-vivo expansion of stem cells, comprising the steps of: (a) separating stem cells from other

cells, (b) culturing said separated stem cells with a selective media which contains multi-functional hematopoietic receptor agonist protein(s) and (c) harvesting said stems cells. Stem cells, as well as committed progenitor cells destined to become neutrophils, erythrocytes, platelets, etc. may be distinguished from most other cells by the presence or absence of particular progenitor marker antigens, such as CD34, that are present on the surface of these cells and/or by morphological characteristics. The phenotype for a highly enriched human stem cell fraction is reported as CD34+, Thy-1+ and lin-, but it is to be understood that the present invention is not limited to the expansion of this stem cell population. The CD34+ enriched human stem cell fraction can be separated by a number of reported methods, including affinity columns or beads, magnetic beads or flow cytometry using antibodies directed to surface antigens such as the CD34+. Further, physical separation methods such as counterflow elutriation may be used to enrich hematopoietic progenitors. The CD34+ progenitors are heterogeneous, and may be divided into several sub-populations characterized by the presence or absence of co-expression of different lineage associated cell surface associated molecules. The most immature progenitor cells do not express any known lineage associated markers, such as HLA-DR or CD38, but they may express CD90(thy-1).

Other surface antigens such as CD33, CD38, CD41, CD71, HLA-DR or c-kit can also be used to selectively isolate hematopoietic progenitors. The separated cells can be incubated in selected medium in a culture flask, sterile bag or in hollow fibers. Various colony stimulating factors may be utilized in order to selectively expand cells. Representative factors that have been utilized for ex-vivo expansion of bone marrow include, c-kit ligand, IL-3, G-CSF, GM-CSF, IL-1, IL-6, IL-11, flt-3 ligand or combinations thereof. The proliferation of the stem cells can be monitored by enumerating the number of stem cells and other cells, by standard techniques (e.g. hemacytometer, CFU, LTCIC) or by flow cytometry prior and subsequent to incubation.

[0082] Several methods for ex-vivo expansion of stem cells have been reported utilizing a number of selection methods and expansion using various colony stimulating factors including c-kit ligand (Brandt et al., *Blood* **83**:1507-1514 [1994], McKenna et al., *Blood* **86**:3413-3420 [1995]), IL-3 (Brandt et al., *Blood* **83**:1507-1514 [1994], Sato et al., *Blood* **82**:3600-3609 [1993]), G-CSF (Sato et al., *Blood* **82**:3600-3609 [1993]), GM-CSF (Sato et al., *Blood* **82**:3600-3609 [1993]), IL-1 (Muench et al., *Blood* **81**:3463-3473 [1993]), IL-6 (Sato et al., *Blood* **82**:3600-3609 [1993]), IL-11 (Lemoli et al., *Exp. Hem.* **21**:1668-1672 [1993], Sato et al., *Blood* **82**:3600-3609 [1993]), flt-3

ligand (McKenna et al., *Blood* **86**:3413 3420 [1995]) and/or combinations thereof (Brandt et al., *Blood* **83**:1507 1514 [1994], Haylock et al., *Blood* **80**:1405-1412 [1992], Koller et al., *Biotechnology* **11**:358-363 [1993], (Lemoli et al., *Exp. Hem.* **21**:1668-1672 [1993]), McKenna et al., *Blood* **86**:3413-3420 [1995], Muench et al., *Blood* **81**:3463-3473 [1993], Patchen et al., *Biotherapy* **7**:13-26 [1994], Sato et al., *Blood* **82**:3600-3609 [1993], Smith et al., *Exp. Hem.* **21**:870-877 [1993], Steen et al., *Stem Cells* **12**:214-224 [1994], Tsujino et al., *Exp. Hem.* **21**:1379-1386 [1993]). Among the individual colony stimulating factors, hIL-3 has been shown to be one of the most potent in expanding peripheral blood CD34+ cells (Sato et al., *Blood* **82**:3600-3609 [1993], Kobayashi et al., *Blood* **73**:1836-1841 [1989]). However, no single factor has been shown to be as effective as the combination of multiple factors. The present invention provides methods for ex vivo expansion that utilize multi-functional hematopoietic receptor agonists that are more effective than a single factor alone.

[0083] Another aspect of the invention provides methods of sustaining and/or expanding hematopoietic precursor cells which includes inoculating the cells into a culture vessel which contains a culture medium that has been conditioned by exposure to a stromal cell line such as HS-5 (WO 96/02662, Roecklein and Torok-Strob, *Blood* **85**:997-1105, 1995) that has

been supplemented with a multi-functional hematopoietic receptor agonist of the present invention.

[0084] Another projected clinical use of growth factors has been in the in vitro activation of hematopoietic progenitors and stem cells for gene therapy. Due to the long life-span of hematopoietic progenitor cells and the distribution of their daughter cells throughout the entire body, hematopoietic progenitor cells are good candidates for ex vivo gene transfection. In order to have the gene of interest incorporated into the genome of the hematopoietic progenitor or stem cell one needs to stimulate cell division and DNA replication. Hematopoietic stem cells cycle at a very low frequency which means that growth factors may be useful to promote gene transduction and thereby enhance the clinical prospects for gene therapy. Potential applications of gene therapy (review Crystal, *Science* **270**:404-410 [1995]) include; 1) the treatment of many congenital metabolic disorders and immunodeficiencies (Kay and Woo, *Trends Genet.* **10**:253-257 [1994]), 2) neurological disorders (Friedmann, *Trends Genet.* **10**:210-214 [1994]), 3) cancer (Culver and Blaese, *Trends Genet.* **10**:174-178 [1994]) and 4) infectious diseases (Gilboa and Smith, *Trends Genet.* **10**:139-144 [1994]).

[0085] There are a variety of methods, known to those with skill in the art, for introducing genetic material into a host

cell. A number of vectors, both viral and non-viral have been developed for transferring therapeutic genes into primary cells. Viral based vectors include; 1) replication deficient recombinant retrovirus (Boris-Lawrie and Temin, *Curr. Opin. Genet. Dev.* **3**:102-109 [1993], Boris-Lawrie and *Temin, Annal. New York Acad. Sci.* **716**:59-71 [1994], Miller, *Current Top. Microbiol. Immunol.* **158**:1-24 [1992]) and replication-deficient recombinant adenovirus (Berkner, *BioTechniques* **6**:616-629 [1988], Berkner, *Current Top. Microbiol. Immunol.* **158**:39-66 [1992], Brody and Crystal, *Annal. New York Acad. Sci.* **716**:90-103 [1994]). Non-viral based vectors include protein/DNA complexes (Cristiano et al., *PNAS USA.* **90**:2122-2126 [1993], Curiel et al., *PNAS USA* **88**:8850-8854 [1991], Curiel, *Annal. New York Acad. Sci.* **716**:36-58 [1994]), electroporation and liposome mediated delivery such as cationic liposomes (Farhood et al., *Annal. New York Acad. Sci.* **716**:23-35 [1994]).

[0086] The present invention provides an improvement to the existing methods of expanding hematopoietic cells, which new genetic material has been introduced, in that it provides methods utilizing multi-functional hematopoietic receptor agonist proteins that have improved biological activity, including an activity not seen by any single colony stimulation factor.

[0087] Many drugs may cause bone marrow suppression or hematopoietic deficiencies. Examples of such drugs are AZT, DDI, alkylating agents and anti-metabolites used in chemotherapy, antibiotics such as chloramphenicol, penicillin, gancyclovir, daunomycin and sulfa drugs, phenothiazones, tranquilizers such as meprobamate, analgesics such as aminopyrine and dipyrone, anti-convulsants such as phenytoin or carbamazepine, antithyroids such as propylthiouracil and methimazole and diuretics. The multi-functional hematopoietic receptor agonists of the present invention may be useful in preventing or treating the bone marrow suppression or hematopoietic deficiencies which often occur in patients treated with these drugs.

[0088] Hematopoietic deficiencies may also occur as a result of viral, microbial or parasitic infections and as a result of treatment for renal disease or renal failure, e.g., dialysis. The multi-functional hematopoietic receptor agonists of the present invention may be useful in treating such hematopoietic deficiencies.

[0089] The treatment of hematopoietic deficiency may include administration of a pharmaceutical composition containing the multi-functional hematopoietic receptor agonists to a patient. The multi-functional hematopoietic receptor agonists of the present invention may also be useful

for the activation and amplification of hematopoietic precursor cells by treating these cells in vitro with the multi-functional hematopoietic receptor agonist proteins of the present invention prior to injecting the cells into a patient.

[0090] Various immunodeficiencies, e.g., in T and/or B lymphocytes, or immune disorders, e.g., rheumatoid arthritis, may also be beneficially affected by treatment with the multi-functional hematopoietic receptor agonists of the present invention. Immunodeficiencies may be the result of viral infections, e.g., HTLVI, HTLVII, HTLVIII, severe exposure to radiation, cancer therapy or the result of other medical treatment. The multi-functional hematopoietic receptor agonists of the present invention may also be employed, alone or in combination with other colony stimulating factors, in the treatment of other blood cell deficiencies, including thrombocytopenia (platelet deficiency), or anemia. Other uses for these novel polypeptides are the in vivo and ex vivo treatment of patients recovering from bone marrow transplants, and in the development of monoclonal and polyclonal antibodies generated by standard methods for diagnostic or therapeutic use.

[0091] Other aspects of the present invention are methods and therapeutic compositions for treating the conditions

referred to above. Such compositions comprise a therapeutically effective amount of one or more of the multi-functional hematopoietic receptor agonists of the present invention in a mixture with a pharmaceutically acceptable carrier. This composition can be administered either parenterally, intravenously or subcutaneously. When administered, the therapeutic composition for use in this invention is preferably in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such a parenterally acceptable protein solution, having due regard to pH, isotonicity, stability and the like, is within the skill of the art.

[0092] The dosage regimen involved in a method for treating the above-described conditions will be determined by the attending physician considering various factors which modify the action of drugs, e.g., the condition, body weight, sex and diet of the patient, the severity of any infection, time of administration and other clinical factors. Generally, a daily regimen may be in the range of 0.2 - 150 μg/kg of multi-functional hematopoietic receptor agonist protein per kilogram of body weight. Dosages would be adjusted relative to the activity of a given multi-functional hematopoietic receptor agonist protein and it would not be unreasonable to note that dosage regimens may include doses as low as 0.1 microgram and

as high as 1 milligram per kilogram of body weight per day. In addition, there may exist specific circumstances where dosages of multi-functional hematopoietic receptor agonist would be adjusted higher or lower than the range of 0.2 - 150 micrograms per kilogram of body weight. These include co-administration with other colony stimulating factors or IL-3 variants or growth factors; co-administration with chemotherapeutic drugs and/or radiation; the use of glycosylated multi-functional hematopoietic receptor agonist protein; and various patient-related issues mentioned earlier in this section. As indicated above, the therapeutic method and compositions may also include co-administration with other human factors. A non-exclusive list of other appropriate colony stimulating factors (CSFs), cytokines, lymphokines, hematopoietic growth factors and interleukins for simultaneous or serial co-administration with the polypeptides of the present invention includes GM-CSF, G-CSF, c-mpl ligand (also known as TPO or MGDF), M-CSF, erythropoietin (EPO), IL-1, IL-4, IL-2, IL-3, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-15, IL-16, LIF, flt3 ligand, and stem cell factor (SCF) also known as steel factor or c-kit ligand, or combinations thereof. The dosage recited above would be adjusted to compensate for such additional components in the therapeutic composition. Progress of the treated patient can

be monitored by periodic assessment of the hematological profile, e.g., differential cell count and the like.

MATERIALS AND METHODS

[0093] Unless noted otherwise, all specialty chemicals were obtained from Sigma, Co. (St. Louis, MO). Restriction endonucleases and T4 DNA ligase were obtained from New England Biolabs (Beverly, MA) or Boehringer Mannheim (Indianapolis, IN).

Transformation of *E. coli* strains

[0094] *E. coli* strains, such as DH5á™ (Life Technologies, Gaithersburg, MD) and TG1 (Amersham Corp., Arlington Heights, IL) are used for transformation of ligation reactions and are the source of plasmid DNA for transfecting mammalian cells. *E. coli* strains, such as JM101 (Yanisch-Perron, et al., *Gene*, 33: 103-119, 1985) and MON105 (Obukowicz, et al., *Appl. and Envir. Micr.*, 58: 1511-1523, 1992) can be used for expressing the multi-functional hematopoietic receptor agonist of the present invention in the cytoplasm or periplasmic space.

MON105 ATCC#55204: F-, lambda-,IN(rrnD, rrE)1, rpoD+, rpoH358

DH5á™: F-, phi80dlacZdeltaM15, delta(lacZYA-argF)U169, deoR, recA1, endA1, hsdR17(rk-,mk+), phoA, supE44lamda-, thi-1, gyrA96, relA1

TG1: delta(lac-pro), supE, thi-1, hsdD5/F'(traD36, proA+B+, lacIq, lacZdeltaM15)

JM101 ATCC#33876: delta (pro lac), *sup*E, *thi*, F'(*tra*D36, proA+B+, *lac*Iq, *lac*ZdeltaM15)

[0095] DH5á™ Subcloning efficiency cells are purchased as competent cells and are ready for transformation using the manufacturer's protocol, while both *E. coli* strains TG1 and MON105 are rendered competent to take up DNA using a CaCl2 method. Typically, 20 to 50 mL of cells are grown in LB medium (1% bacto-tryptone, 0.5% bacto-yeast extract, 150 mM NaCl) to a density of approximately 1.0 optical density unit at 600 nanometers (OD600) as measured by a Baush & Lomb Spectronic spectrophotometer (Rochester, NY). The cells are collected by centrifugation and resuspended in one-fifth culture volume of CaCl2 solution (50 mM CaCl2, 10 mM Tris-Cl, pH7.4) and are held at 4°C for 30 minutes. The cells are again collected by centrifugation and resuspended in one-tenth culture volume of CaCl2 solution. Ligated DNA is added to 0.2 mL of these cells, and the samples are held at 4°C for 30-60 minutes. The samples are shifted to 42°C for two minutes and 1.0 mL of LB is added prior to shaking the samples at 37°C for one hour. Cells from these samples are spread on plates (LB medium plus 1.5% bacto-agar) containing either ampicillin (100 micrograms/mL, ug/mL) when selecting for ampicillin-resistant transformants, or spectinomycin (75 ug/mL) when selecting for spectinomycin-resistant transformants. The plates are

incubated overnight at 37°C. Colonies are picked and inoculated into LB plus appropriate antibiotic (100 ug/mL ampicillin or 75 ug/mL spectinomycin) and are grown at 37°C while shaking.

Methods For Creation of Genes With New N-Terminus/C-Terminus

Method I. Creation of genes with new N-terminus/C-terminus which contain a linker region (L_2).

[0096] Genes with new N-terminus/C-terminus which contain a linker region (L_2) separating the original C-terminus and N-terminus can be made essentially following the method described in L. S. Mullins, et al *J. Am. Chem. Soc.* **116**, 5529-5533, 1994). Multiple steps of polymerase chain reaction (PCR) amplifications are used to rearrange the DNA sequence encoding the primary amino acid sequence of the protein. The steps are illustrated in Figure 2.

[0097] In the first step, the first primer set ("new start" and "linker start") is used to create and amplify, from the original gene sequence, the DNA fragment ("Fragment Start") that contains the sequence encoding the new N-terminal portion of the new protein followed by the linker (L_2) that connects the C-terminal and N-terminal ends of the original protein. In the second step, the second primer set ("new stop" and "linker stop") is used to create and amplify, from the original gene

sequence, the DNA fragment ("Fragment Stop") that encodes the same linker as used above, followed by the new C-terminal portion of the new protein. The "new start" and "new stop" primers are designed to include the appropriate restriction sites which allow cloning of the new gene into expression plasmids. Typical PCR conditions are one cycle 95°C melting for two minutes; 25 cycles 94°C denaturation for one minute, 50°C annealing for one minute and 72°C extension for one minute; plus one cycle 72°C extension for seven minutes. A Perkin Elmer GeneAmp PCR Core Reagents kit is used. A 100 ul reaction contains 100 pmole of each primer and one ug of template DNA; and 1x PCR buffer, 200 uM dGTP, 200 uM dATP, 200 uM dTTP, 200 uM dCTP, 2.5 units AmpliTaq DNA polymerase and 2 mM MgCl2. PCR reactions are performed in a Model 480 DNA thermal cycler (Perkin Elmer Corporation, Norwalk, CT).

[0098] "Fragment Start" and "Fragment Stop", which have complementary sequence in the linker region and the coding sequence for the two amino acids on both sides of the linker, are joined together in a third PCR step to make the full-length gene encoding the new protein. The DNA fragments "Fragment Start" and "Fragment Stop" are resolved on a 1% TAE gel, stained with ethidium bromide and isolated using a Qiaex Gel Extraction kit (Qiagen). These fragments are combined in equimolar quantities, heated at 70°C for ten minutes and slow

cooled to allow annealing through their shared sequence in "linker start" and "linker stop". In the third PCR step, primers "new start" and "new stop" are added to the annealed fragments to create and amplify the full-length new N-terminus/C-terminus gene. Typical PCR conditions are one cycle 95°C melting for two minutes; 25 cycles 94°C denaturation for one minute, 60°C annealing for one minute and 72°C extension for one minute; plus one cycle 72°C extension for seven minutes. A Perkin Elmer GeneAmp PCR Core Reagents kit is used. A 100 ul reaction contains 100 pmole of each primer and approximately 0.5 ug of DNA; and 1x PCR buffer, 200 uM dGTP, 200 uM dATP, 200 uM dTTP, 200 uM dCTP, 2.5 units AmpliTaq DNA polymerase and 2 mM MgCl2. PCR reactions are purified using a Wizard PCR Preps kit (Promega).

Method II.
Creation of genes with new
N-terminus/C-terminus without a linker region.

[0099] New N-terminus/C-terminus genes without a linker joining the original N-terminus and C-terminus can be made using two steps of PCR amplification and a blunt end ligation. The steps are illustrated in Figure 3. In the first step, the primer set ("new start" and "P-bl start") is used to create and amplify, from the original gene sequence, the DNA fragment ("Fragment Start") that contains the sequence encoding the new N-terminal portion of the new protein. In the second step,

the primer set ("new stop" and "P-bl stop") is used to create and amplify, from gene sequence, the DNA fragment ("Fragment Stop") that contains the sequence encoding the new C-terminal portion of the new protein. The "new start" and "new stop" primers are designed to include appropriate restriction sites which allow cloning of the new gene into expression vectors. Typical PCR conditions are one cycle 95°C melting for two minutes; 25 cycles 94°C denaturation for one minute, 50°C annealing for 45 seconds and 72°C extension for 45 seconds. Deep Vent polymerase (New England Biolabs) is used to reduce the occurrence of overhangs in conditions recommended by the manufacturer. The "P-bl start" and "P-bl stop" primers are phosphorylated at the 5' end to aid in the subsequent blunt end ligation of "Fragment Start" and "Fragment Stop" to each other. A 100 ul reaction contained 150 pmole of each primer and one ug of template DNA; and 1x Vent buffer (New England Biolabs), 300 uM dGTP, 300 uM dATP, 300 uM dTTP, 300 uM dCTP, and 1 unit Deep Vent polymerase. PCR reactions are performed in a Model 480 DNA thermal cycler (Perkin Elmer Corporation, Norwalk, CT). PCR reaction products are purified using a Wizard PCR Preps kit (Promega).

[00100] The primers are designed to include appropriate restriction sites which allow for the cloning of the new gene into expression vectors. Typically "Fragment Start" is

designed to create NcoI restriction site , and "Fragment Stop" is designed to create a HindIII restriction site. Restriction digest reactions are purified using a Magic DNA Clean-up System kit (Promega). Fragments Start and Stop are resolved on a 1% TAE gel, stained with ethidium bromide and isolated using a Qiaex Gel Extraction kit (Qiagen). These fragments are combined with and annealed to the ends of the ~ 3800 base pair NcoI/HindIII vector fragment of pMON3934 by heating at 50°C for ten minutes and allowed to slow cool. The three fragments are ligated together using T4 DNA ligase (Boehringer Mannheim). The result is a plasmid containing the full-length new N-terminus/C-terminus gene. A portion of the ligation reaction is used to transform *E. coli* strain DH5á cells (Life Technologies, Gaithersburg, MD). Plasmid DNA is purified and sequence confirmed as below.

Method III.
Creation of new N-terminus/C-terminus
genes by tandem-duplication method

[0100] New N-terminus/C-terminus genes can be made based on the method described in R. A. Horlick, et al *Protein Eng.* **5**:427-431, 1992). Polymerase chain reaction (PCR) amplification of the new N-terminus/C-terminus genes is performed using a tandemly duplicated template DNA. The steps are illustrated in Figure 3.

[0101] The tandemly-duplicated template DNA is created by cloning and contains two copies of the gene separated by DNA sequence encoding a linker connecting the original C- and N-terminal ends of the two copies of the gene. Specific primer sets are used to create and amplify a full-length new N terminus/C-terminus gene from the tandemly-duplicated template DNA. These primers are designed to include appropriate restriction sites which allow for the cloning of the new gene into expression vectors. Typical PCR conditions are one cycle 95°C melting for two minutes; 25 cycles 94°C denaturation for one minute, 50°C annealing for one minute and 72°C extension for one minute; plus one cycle 72°C extension for seven minutes. A Perkin Elmer GeneAmp PCR Core Reagents kit (Perkin Elmer Corporation, Norwalk, CT) is used. A 100 ul reaction contains 100 pmole of each primer and one ug of template DNA; and 1x PCR buffer, 200 uM dGTP, 200 uM dATP, 200 uM dTTP, 200 uM dCTP, 2.5 units AmpliTaq DNA polymerase and 2 mM $MgCl_2$. PCR reactions are performed in a Model 480 DNA thermal cycler (Perkin Elmer Corporation, Norwalk, CT). PCR reactions are purified using a Wizard PCR Preps kit (Promega).

Cloning of new N-terminus/C-terminus genes
into multi-functional receptor agonist expression vectors.

[0102] The new N-terminus/C-terminus gene is digested with restriction endonucleases to create ends that are compatible

to insertion into an expression vector containing another colony stimulating factor gene. This expression vector is likewise digested with restriction endonucleases to form compatible ends. After purification, the gene and the vector DNAs are combined and ligated using T4 DNA ligase. A portion of the ligation reaction is used to transform E. coli. Plasmid DNA is purified and sequenced to confirm the correct insert. The correct clones are grown for protein expression.

DNA isolation and characterization

[0103] Plasmid DNA can be isolated by a number of different methods and using commercially available kits known to those skilled in the art. A few such methods are shown herein. Plasmid DNA is isolated using the Promega Wizard™ Miniprep kit (Madison, WI), the Qiagen QIAwell Plasmid isolation kits (Chatsworth, CA) or Qiagen Plasmid Midi kit. These kits follow the same general procedure for plasmid DNA isolation. Briefly, cells are pelleted by centrifugation (5000 x g), plasmid DNA released with sequential NaOH/acid treatment, and cellular debris is removed by centrifugation (10000 x g). The supernatant (containing the plasmid DNA) is loaded onto a column containing a DNA-binding resin, the column is washed, and plasmid DNA eluted with TE. After screening for the colonies with the plasmid of interest, the *E. coli* cells are inoculated into 50-100 mls of LB plus appropriate antibiotic

for overnight growth at 37°C in an air incubator while shaking. The purified plasmid DNA is used for DNA sequencing, further restriction enzyme digestion, additional subcloning of DNA fragments and transfection into mammalian, *E. coli* or other cells.

Sequence confirmation.

[0104] Purified plasmid DNA is resuspended in dH_2O and quantitated by measuring the absorbance at 260/280 nm in a Bausch and Lomb Spectronic 601 UV spectrometer. DNA samples are sequenced using ABI PRISM™ DyeDeoxy™ terminator sequencing chemistry (Applied Biosystems Division of Perkin Elmer Corporation, Lincoln City, CA) kits (Part Number 401388 or 402078) according to the manufacturers suggested protocol usually modified by the addition of 5% DMSO to the sequencing mixture. Sequencing reactions are performed in a Model 480 DNA thermal cycler (Perkin Elmer Corporation, Norwalk, CT) following the recommended amplification conditions. Samples are purified to remove excess dye terminators with Centri-Sep™ spin columns (Princeton Separations, Adelphia, NJ) and lyophilized. Fluorescent dye labeled sequencing reactions are resuspended in deionized formamide, and sequenced on denaturing 4.75% polyacrylamide-8M urea gels using an ABI Model 373A automated DNA sequencer. Overlapping DNA sequence fragments are analyzed and assembled into master DNA contigs

using Sequencher v2.1 DNA analysis software (Gene Codes Corporation, Ann Arbor, MI).

Expression of multi-functional receptor agonists in mammalian cells

Mammalian Cell Transfection/Production of Conditioned Media

[0105] The BHK-21 cell line can be obtained from the ATCC (Rockville, MD). The cells are cultured in Dulbecco's modified Eagle media (DMEM/high-glucose), supplemented to 2 mM (mM) L-glutamine and 10% fetal bovine serum (FBS). This formulation is designated BHK growth media. Selective media is BHK growth media supplemented with 453 units/mL hygromycin B (Calbiochem, San Diego, CA). The BHK-21 cell line was previously stably transfected with the HSV transactivating protein VP16, which transactivates the IE110 promoter found on the plasmid pMON3359 (See Hippenmeyer et al., *Bio/Technology*, pp.1037-1041, 1993). The VP16 protein drives expression of genes inserted behind the IE110 promoter. BHK-21 cells expressing the transactivating protein VP16 are designated BHK-VP16. The plasmid pMON1118 (See Highkin et al., *Poultry Sci.*, **70**: 970-981, 1991) expresses the hygromycin resistance gene from the SV40 promoter. A similar plasmid is available from ATCC, pSV2-hph.

[0106] BHK-VP16 cells are seeded into a 60 millimeter (mm) tissue culture dish at 3 X 10^5 cells per dish 24 hours prior

to transfection. Cells are transfected for 16 hours in 3 mL of "OPTIMEM"™ (Gibco-BRL, Gaithersburg, MD) containing 10 ug of plasmid DNA containing the gene of interest, 3 ug hygromycin resistance plasmid, pMON1118, and 80 ug of Gibco-BRL "LIPOFECTAMINE"™ per dish. The media is subsequently aspirated and replaced with 3 mL of growth media. At 48 hours post-transfection, media from each dish is collected and assayed for activity (transient conditioned media). The cells are removed from the dish by trypsin-EDTA, diluted 1:10 and transferred to 100 mm tissue culture dishes containing 10 mL of selective media. After approximately 7 days in selective media, resistant cells grow into colonies several millimeters in diameter. The colonies are removed from the dish with filter paper (cut to approximately the same size as the colonies and soaked in trypsin/EDTA) and transferred to individual wells of a 24 well plate containing 1 mL of selective media. After the clones are grown to confluence, the conditioned media is re-assayed, and positive clones are expanded into growth media.

Expression of multi-functional receptor agonists in *E. coli*

[0107] *E. coli* strain MON105 or JM101 harboring the plasmid of interest are grown at 37°C in M9 plus casamino acids medium with shaking in a air incubator Model G25 from New Brunswick

Scientific (Edison, New Jersey). Growth is monitored at OD600 until it reaches a value of 1.0 at which time Nalidixic acid (10 milligrams/mL) in 0.1 N NaOH is added to a final concentration of 50 µg/mL. The cultures are then shaken at 37°C for three to four additional hours. A high degree of aeration is maintained throughout culture period in order to achieve maximal production of the desired gene product. The cells are examined under a light microscope for the presence of inclusion bodies (IB). One mL aliquots of the culture are removed for analysis of protein content by boiling the pelleted cells, treating them with reducing buffer and electrophoresis via SDS-PAGE (see Maniatis et al. Molecular Cloning: A Laboratory Manual, 1982). The culture is centrifuged (5000 x g) to pellet the cells.

Inclusion Body preparation, Extraction, Refolding, Dialysis, DEAE Chromatography, and Characterization of the multi-functional hematopoietic receptor agonists which accumulate as inclusion bodies in *E. coli*.

Isolation of Inclusion Bodies:

[0108] The cell pellet from a 330 mL *E. coli* culture is resuspended in 15 mL of sonication buffer (10 mM 2-amino-2-(hydroxymethyl) 1,3-propanediol hydrochloride (Tris-HCl), pH 8.0 + 1 mM ethylenediaminetetraacetic acid (EDTA). These resuspended cells are sonicated using the microtip probe of a Sonicator Cell Disruptor (Model W-375, Heat Systems-

Ultrasonics, Inc., Farmingdale, New York). Three rounds of sonication in sonication buffer followed by centrifugation are employed to disrupt the cells and wash the inclusion bodies (IB). The first round of sonication is a 3 minute burst followed by a 1 minute burst, and the final two rounds of sonication are for 1 minute each.

Extraction and refolding of proteins from inclusion body pellets:

[0109] Following the final centrifugation step, the IB pellet is resuspended in 10 mL of 50 mM Tris-HCl, pH 9.5, 8 M urea and 5 mM dithiothreitol (DTT) and stirred at room temperature for approximately 45 minutes to allow for denaturation of the expressed protein.

[0110] The extraction solution is transferred to a beaker containing 70 mL of 5 mM Tris-HCl, pH 9.5 and 2.3 M urea and gently stirred while exposed to air at 4°C for 18 to 48 hours to allow the proteins to refold. Refolding is monitored by analysis on a Vydac (Hesperia, Ca.) C18 reversed phase high pressure liquid chromatography (RP-HPLC) column (0.46x25 cm). A linear gradient of 40% to 65% acetonitrile, containing 0.1% trifluoroacetic acid (TFA), is employed to monitor the refold. This gradient is developed over 30 minutes at a flow rate of 1.5 mL per minute. Denatured proteins generally elute later in the gradient than the refolded proteins.

Purification

[0111] Following the refold, contaminating *E. coli* proteins are removed by acid precipitation. The pH of the refold solution is titrated to between pH 5.0 and pH 5.2 using 15% (v/v) acetic acid (HOAc). This solution is stirred at 4°C for 2 hours and then centrifuged for 20 minutes at 12,000 x g to pellet any insoluble protein.

[0112] The supernatant from the acid precipitation step is dialyzed using a Spectra/Por 3 membrane with a molecular weight cut off (MWCO) of 3,500 daltons. The dialysis is against 2 changes of 4 liters (a 50-fold excess) of 10 mM Tris-HCl, pH 8.0 for a total of 18 hours. Dialysis lowers the sample conductivity and removes urea prior to DEAE chromatography. The sample is then centrifuged (20 minutes at 12,000 x g) to pellet any insoluble protein following dialysis.

[0113] A Bio-Rad Bio-Scale DEAE2 column (7 x 52 mm) is used for ion exchange chromatography. The column is equilibrated in a buffer containing 10 mM Tris-HCl, pH 8.0, and a 0-to-500 mM sodium chloride (NaCl) gradient, in equilibration buffer, over 45 column volumes is used to elute the protein. A flow rate of 1.0 mL per minute is used throughout the run. Column fractions (2.0 mL per fraction) are collected across the gradient and analyzed by RP HPLC on a Vydac (Hesperia, Ca.)

C18 column (0.46 x 25 cm). A linear gradient of 40% to 65% acetonitrile, containing 0.1% trifluoroacetic acid (TFA), is employed. This gradient is developed over 30 minutes at a flow rate of 1.5 mL per minute. Pooled fractions are then dialyzed against 2 changes of 4 liters (50-to-500-fold excess) of 10 mM ammonium acetate (NH4Ac), pH 4.0 for a total of 18 hours. Dialysis is performed using a Spectra/Por 3 membrane with a MWCO of 3,500 daltons. Finally, the sample is sterile filtered using a 0.22µm syringe filter (µStar LB syringe filter, Costar, Cambridge, Ma.), and stored at 4°C.

[0114] In some cases the folded proteins can be affinity purified using affinity reagents such as mAbs or receptor subunits attached to a suitable matrix. Alternatively, (or in addition) purification can be accomplished using any of a variety of chromatographic methods such as: ion exchange, gel filtration or hydrophobic chromatography or reversed phase HPLC.

[0115] These and other protein purification methods are described in detail in Methods in Enzymology, Volume 182 'Guide to Protein Purification' edited by Murray Deutscher, Academic Press, San Diego, CA (1990).

Protein Characterization:

[0116] The purified protein is analyzed by RP-HPLC, electrospray mass spectrometry, and SDS-PAGE. The protein

quantitation is done by amino acid composition, RP-HPLC, and Bradford protein determination. In some cases tryptic peptide mapping is performed in conjunction with electrospray mass spectrometry to confirm the identity of the protein.

AML Proliferation Assay for
Bioactive Human Interleukin-3

[0117] The factor-dependent cell line AML 193 was obtained from the American Type Culture Collection (ATCC, Rockville, MD). This cell line, established from a patient with acute myelogenous leukemia, is a growth factor dependent cell line which displayed enhanced growth in GM-CSF supplemented medium (Lange, B., et al., *Blood* **70**: 192, 1987; Valtieri, M., et al., *J. Immunol.* **138**:4042, 1987). The ability of AML 193 cells to proliferate in the presence of human IL-3 has also been documented. (Santoli, D., et al., *J. Immunol.* **139**: 348, 1987). A cell line variant was used, AML 193 1.3, which was adapted for long term growth in IL-3 by washing out the growth factors and starving the cytokine dependent AML 193 cells for growth factors for 24 hours. The cells are then replated at $1x10^5$ cells/well in a 24 well plate in media containing 100 U/mL IL-3. It took approximately 2 months for the cells to grow rapidly in IL-3. These cells are maintained as AML 193 1.3 thereafter by supplementing tissue culture medium (see below) with human IL-3.

[0118] AML 193 1.3 cells are washed 6 times in cold Hanks balanced salt solution (HBSS, Gibco, Grand Island, NY) by centrifuging cell suspensions at 250 x g for 10 minutes followed by decantation of the supernatant. Pelleted cells are resuspended in HBSS and the procedure is repeated until six wash cycles are completed. Cells washed six times by this procedure are resuspended in tissue culture medium at a density ranging from 2×10^5 to 5×10^5 viable cells/mL. This medium is prepared by supplementing Iscove's modified Dulbecco's Medium (IMDM, Hazelton, Lenexa, KS) with albumin, transferrin, lipids and 2-mercaptoethanol. Bovine albumin (Boehringer-Mannheim, Indianapolis, IN) is added at 500 µg/mL; human transferrin (Boehringer-Mannheim, Indianapolis, IN) is added at 100 µg/mL; soybean lipid (Boehringer-Mannheim, Indianapolis, IN) is added at 50 µg/mL; and 2-mercaptoethanol (Sigma, St. Louis, MO) is added at 5×10^{-5} M.

[0119] Serial dilutions of human interleukin-3 or multi-functional hematopoietic receptor agonist proteins are made in triplicate series in tissue culture medium supplemented as stated above in 96 well Costar 3596 tissue culture plates. Each well contained 50 µl of medium containing interleukin-3 or multi-functional hematopoietic receptor agonist proteins once serial dilutions are completed. Control wells contained tissue culture medium alone (negative control). AML 193 1.3

cell suspensions prepared as above are added to each well by pipetting 50 µl (2.5 x 10^4 cells) into each well. Tissue culture plates are incubated at 37°C with 5% CO_2 in humidified air for 3 days. On day 3, 0.5 µCi ^{3}H-thymidine (2 Ci/mM, New England Nuclear, Boston, MA) is added in 50 µl of tissue culture medium. Cultures are incubated at 37°C with 5% CO_2 in humidified air for 18-24 hours. Cellular DNA is harvested onto glass filter mats (Pharmacia LKB, Gaithersburg, MD) using a TOMTEC cell harvester (TOMTEC, Orange, CT) which utilized a water wash cycle followed by a 70% ethanol wash cycle. Filter mats are allowed to air dry and then placed into sample bags to which scintillation fluid (Scintiverse II, Fisher Scientific, St. Louis, MO or BetaPlate Scintillation Fluid, Pharmacia LKB, Gaithersburg, MD) is added. Beta emissions of samples from individual tissue culture wells are counted in a LKB BetaPlate model 1205 scintillation counter (Pharmacia LKB, Gaithersburg, MD) and data is expressed as counts per minute of ^{3}H-thymidine incorporated into cells from each tissue culture well. Activity of each human interleukin-3 preparation or multi-functional hematopoietic receptor agonist protein preparation is quantitated by measuring cell proliferation (^{3}H-thymidine incorporation) induced by graded concentrations of interleukin-3 or multi-functional hematopoietic receptor agonist. Typically, concentration

ranges from 0.05 pM - 10^5 pM are quantitated in these assays. Activity is determined by measuring the dose of interleukin-3 or multi-functional hematopoietic receptor agonist protein which provides 50% of maximal proliferation (EC_{50} = 0.5 x (maximum average counts per minute of ^3H-thymidine incorporated per well among triplicate cultures of all concentrations of interleukin-3 tested - background proliferation measured by ^3H-thymidine incorporation observed in triplicate cultures lacking interleukin-3). This EC_{50} value is also equivalent to 1 unit of bioactivity. Every assay is performed with native interleukin-3 as a reference standard so that relative activity levels could be assigned.

[0120] Typically, the multi-functional hematopoietic receptor agonist proteins were tested in a concentration range of 2000 pM to 0.06 pM titrated in serial 2 fold dilutions.

[0121] Activity for each sample was determined by the concentration which gave 50% of the maximal response by fitting a four-parameter logistic model to the data. It was observed that the upper plateau (maximal response) for the sample and the standard with which it was compared did not differ. Therefore relative potency calculation for each sample was determined from EC50 estimations for the sample and the standard as indicated above. AML 193.1.3 cells proliferate in response to hIL-3, hGM-CSF and hG-CSF. Therefore the

following additional assays were performed for some samples to demonstrate that the G-CSF receptor agonist portion of the multi-functional hematopoietic receptor agonist proteins was active. The proliferation assay was performed with the multi-functional hematopoietic receptor agonist plus and minus neutralizing monoclonal antibodies to the hIL-3 receptor agonist portion. In addition, a fusion molecule with the factor Xa cleavage site was cleaved then purified and the halves of the molecule were assayed for proliferative activity. These experiments showed that both components of the multi-functional hematopoietic receptor agonist proteins were active.

TF1 c-mpl ligand dependent proliferation assay

[0122] The c-mpl ligand proliferative activity can be assayed using a subclone of the pluripotential human cell line TF1 (Kitamura et al., J. Cell Physiol 140:323-334. [1989]). TF1 cells are maintained in h-IL3 (100 U/mL). To establish a sub-clone responsive to c-mpl ligand, cells are maintained in passage media containing 10% supernatant from BHK cells transfected with the gene expressing the 1-153 form of c-mpl ligand (pMON26448). Most of the cells die, but a subset of cells survive. After dilution cloning, a c-mpl ligand responsive clone is selected, and these cells are split into passage media to a density of 0.3×10^6 cells/mL the day prior

to assay set-up. Passage media for these cells is the following: RPMI 1640 (Gibco), 10% FBS (Harlan, Lot #91206), 10% c-mpl ligand supernatant from transfected BHK cells, 1 mM sodium pyruvate (Gibco), 2 mM glutamine (Gibco), and 100 ug/mL penicillin-streptomycin (Gibco). The next day, cells are harvested and washed twice in RPMI or IMDM media with a final wash in the ATL, or assay media. ATL medium consists of the following:IMDM (Gibco), 500 ug/mL of bovine serum albumin, 100 ug/mL of human transferrin, 50 ug/mL soybean lipids, 4 x 10-8M beta-mercaptoethanol and 2 mL of A9909 (Sigma, antibiotic solution) per 1000 mL of ATL. Cells are diluted in assay media to a final density of 0.25 x 10^6 cells/mL in a 96-well low evaporation plate (Costar) to a final volume of 50 ul. Transient supernatants (conditioned media) from transfected clones are added at a volume of 50 ul as duplicate samples at a final concentration of 50% and diluted three-fold to a final dilution of 1.8%. Triplicate samples of a dose curve of IL-3 variant pMON13288 starting at 1 ng/mL and diluted using three-fold dilutions to 0.0014ng/mL is included as a positive control. Plates are incubated at 5% CO_2 and 37° C. At day six of culture, the plate is pulsed with 0.5 Ci of 3H/well (NEN) in a volume of 20 ul/well and allowed to incubate at 5% CO_2 and 37° C for four hours. The plate is harvested and counted on a Betaplate counter.

Other in vitro cell based proliferation assays

[0123] Other in vitro cell based assays, known to those skilled in the art, may also be useful to determine the activity of the multi-functional hematopoietic receptor agonists depending on the factors that comprise the molecule in a similar manner as described in the AML 193.1.3 cell proliferation assay. The following are examples of other useful assays.

TF1 proliferation assay: TF1 is a pluripotential human cell line (Kitamura et al., J. Cell Physiol 140:323-334. [1989]) that responds to hIL-3.

32D proliferation assay: 32D is a murine IL-3 dependent cell line which does not respond to human IL-3 but does respond to human G-CSF which is not species restricted.

Baf/3 proliferation assay: Baf/3 is a murine IL-3 dependent cell line which does not respond to human IL-3 or human c-mpl ligand but does respond to human G-CSF which is not species restricted.

T1165 proliferation assay: T1165 cells are a IL-6 dependent murine cell line (Nordan et al., 1986) which respond to IL-6 and IL-11.

Human Plasma Clot meg-CSF Assay: Used to assay megakaryocyte colony formation activity (Mazur et al., 1981).

Transfected cell lines

[0124] Cell lines such as the murine Baf/3 cell line can be transfected with a colony stimulating factor receptor, such as the human G-CSF receptor or human c-mpl receptor, which the cell line does not have. These transfected cell lines can be used to determine the activity of the ligand for which the receptor has been transfected into the cell line.

[0125] One such transfected Baf/3 cell line was made by cloning the cDNA encoding c-mpl from a library made from a c-mpl responsive cell line and cloned into the multiple cloning site of the plasmid pcDNA3 (Invitrogen, San Diego Ca.). Baf/3 cells were transfected with the plasmid via electroporation. The cells were grown under G418 selection in the presence of mouse IL-3 in Wehi conditioned media. Clones were established through limited dilution.

[0126] In a similar manner the human G-CSF receptor can be transfected into the Baf/3 cell line and used to determine the bioactivity of the multi-functional hematopoietic receptor agoinsts.

Analysis of c-mpl ligand proliferative activity

Methods

1. Bone marrow proliferation assay

a. CD34+ Cell Purification:

Bone marrow aspirates (15-20 mL) were obtained from

normal allogeneic marrow donors after informed consent. Cells were diluted 1:3 in phosphate buffered saline (PBS, Gibco-BRL), 30 mL were layered over 15 mL Histopaque-1077 (Sigma) and centrifuged for 30 minutes at 300 RCF. The mononuclear interface layer was collected and washed in PBS. CD34+ cells were enriched from the mononuclear cell preparation using an affinity column per manufacturers instructions (CellPro, Inc, Bothell WA). After enrichment, the purity of CD34+ cells was 70% on average as determined by using flow cytometric analysis using anti-CD34 monoclonal antibody conjugated to fluorescein and anti-CD38 conjugated to phycoerythrin (Becton Dickinson, San Jose CA).

Cells were resuspended at 40,000 cells/mL in X-Vivo 10 media (Bio-Whittaker, Walkersville, MD) and 1 mL was plated in 12-well tissue culture plates (Costar). The growth factor rhIL-3 was added at 100 ng/mL (pMON5873) was added to some wells. hIL3 variants were used at 10 ng/mL to 100 ng/mL. Conditioned media from BHK cells transfected with plasmid encoding c-mpl ligand or multi-functional hematopoietic receptor agonists were tested by addition of 100 µl of supernatant added to 1 mL cultures (approximately a 10% dilution). Cells were incubated at 37°C for 8-14 days at 5% CO_2 in a 37°C humidified incubator.

b. Cell Harvest and Analysis:

At the end of the culture period a total cell count was obtained for each condition. For fluorescence analysis and ploidy determination cells were washed in megakaryocyte buffer (MK buffer, 13.6 mM sodium citrate, 1 mM theophylline, 2.2 µm PGE1, 11 mM glucose, 3% w/v BSA, in PBS, pH 7.4,) (Tomer et al., *Blood* **70**: 1735-1742, 1987) resuspended in 500 µl of MK buffer containing anti-CD41a FITC antibody (1:200, AMAC, Westbrook, ME) and washed in MK buffer. For DNA analysis cells were permeablized in MK buffer containing 0.5% Tween 20 (Fisher, Fair Lawn NJ)for 20 min. on ice followed by fixation in 0.5% Tween-20 and 1% paraformaldehyde (Fisher Chemical) for 30 minutes followed by incubation in propidium iodide (Calbiochem , La Jolla Ca) (50 µg/mL) with RNA-ase (400 U/mL) in 55% v/v MK buffer (200mOsm) for 1-2 hours on ice. Cells were analyzed on a FACScan or Vantage flow cytometer (Becton Dickinson, San Jose, CA). Green fluorescence (CD41a-FITC) was collected along with linear and log signals for red fluorescence (PI) to determine DNA ploidy. All cells were collected to determine the percent of cells that were CD41+. Data analysis was performed using software by LYSIS (Becton Dickinson, San Jose, CA). Percent of cells expressing the CD41 antigen was obtained from flow cytometry analysis(Percent). Absolute (Abs) number of CD41+ cells/mL was calculated by: (Abs)=(Cell Count)*(Percent)/100.

2. Megakaryocyte fibrin clot assay.

CD34+ enriched population were isolated as described above. Cells were suspended at 25,000 cells/mL with or without cytokine(s) in a media consisting of a base Iscoves IMDM media supplemented with 0.3% BSA, 0.4mg/mL apo-transferrin, 6.67μM $FeCl_2$, 25μg/mL $CaCl_2$, 25μg/mL L-asparagine, 500μg/mL e-amino-n-caproic acid and penicillin/streptomycin. Prior to plating into 35mm plates, thrombin was added (0.25 Units/mL) to initiate clot formation. Cells were incubated at 37°C for 13 days at 5% CO_2 in a 37°C humidified incubator.

At the end of the culture period plates were fixed with methanol:acetone (1:3), air dried and stored at -200C until staining. A peroxidase immunocytochemistry staining procedure was used (Zymed, Histostain-SP. San Francisco, CA) using a cocktail of primary monoclonal antibodies consisting of anti-CD41a, CD42 and CD61. Colonies were counted after staining and classified as negative, CFU-MK (small colonies, 1-2 foci and less that approx. 25 cells), BFU-MK (large, multi-foci colonies with > 25 cells) or mixed colonies (mixture of both positive and negative cells.

Methylcellulose Assay

[0127]This assay reflects the ability of colony stimulating factors to stimulate normal bone marrow cells to produce

different types of hematopoietic colonies *in vitro* (Bradley et al., *Aust. Exp Biol. Sci.* **44**:287-300, **1**966), Pluznik et al., *J. Cell Comp. Physio* **66**:319-324, 1965).

Methods

Approximately 30 mL of fresh, normal, healthy bone marrow aspirate are obtained from individuals following informed consent. Under sterile conditions samples are diluted 1:5 with a 1X PBS (#14040.059 Life Technologies, Gaithersburg, MD.) solution in a 50 mL conical tube (#25339-50 Corning, Corning MD). Ficoll (Histopaque 1077 Sigma H-8889) is layered under the diluted sample and centrifuged, 300 x g for 30 min. The mononuclear cell band is removed and washed two times in 1X PBS and once with 1% BSA PBS (CellPro Co., Bothel, WA). Mononuclear cells are counted and CD34+ cells are selected using the Ceprate LC (CD34) Kit (CellPro Co., Bothel, WA) column. This fractionation is performed since all stem and progenitor cells within the bone marrow display CD34 surface antigen.

Cultures are set up in triplicate with a final volume of 1.0 mL in a 35 X 10 mm petri dish (Nunc#174926). Culture medium is purchased from Terry Fox Labs. (HCC-4230 medium (Terry Fox Labs, Vancouver, B.C., Canada) and erythropoietin (Amgen, Thousand Oaks, CA.) is added to the culture media. 3,000-10,000 CD34+ cells are added per dish. Recombinant IL-3,

purified from mammalian cells or *E. coli*, and multi-functional hematopoietic receptor agonist proteins, in conditioned media from transfected mammalian cells or purified from conditioned media from transfected mammalian cells or *E. coli*, are added to give final concentrations ranging from .001 nM to 10 nM. Recombinant hIL-3, GM-CSF, c-mpl ligand and multi-functional hematopoietic receptor agonist are supplied in house. G-CSF (Neupogen) is from Amgen (Thousand Oaks Calf.). Cultures are resuspended using a 3cc syringe and 1.0 mL is dispensed per dish. Control (baseline response) cultures received no colony stimulating factors. Positive control cultures received conditioned media (PHA stimulated human cells: Terry Fox Lab. H2400). Cultures are incubated at 37°C, 5% CO_2 in humidified air.

Hematopoietic colonies which are defined as greater than 50 cells are counted on the day of peak response (days 10-11) using a Nikon inverted phase microscope with a 40x objective combination. Groups of cells containing fewer than 50 cells are referred to as clusters. Alternatively colonies can be identified by spreading the colonies on a slide and stained or they can be picked, resuspended and spun onto cytospin slides for staining.

Human Cord Blood Hemopoietic Growth Factor Assays

[0128]Bone marrow cells are traditionally used for in vitro assays of hematopoietic colony stimulating factor (CSF) activity. However, human bone marrow is not always available, and there is considerable variability between donors. Umbilical cord blood is comparable to bone marrow as a source of hematopoietic stem cells and progenitors (Broxmeyer et al., *PNAS USA* **89**:4109-113, 1992; Mayani et al., *Blood* **81**:3252-3258, 1993). In contrast to bone marrow, cord blood is more readily available on a regular basis. There is also a potential to reduce assay variability by pooling cells obtained fresh from several donors, or to create a bank of cryopreserved cells for this purpose. By modifying the culture conditions, and/or analyzing for lineage specific markers, it is be possible to assay specifically for granulocyte / macrophage colonies (CFU-GM), for megakaryocyte CSF activity, or for high proliferative potential colony forming cell (HPP-CFC) activity.

Methods

Mononuclear cells (MNC) are isolated from cord blood within 24 hr. of collection, using a standard density gradient (1.077 g/mL Histopaque). Cord blood MNC have been further enriched for stem cells and progenitors by several procedures, including immunomagnetic selection for CD14-, CD34+ cells; panning for SBA-, CD34+ fraction using coated flasks from Applied Immune Science (Santa Clara, CA); and CD34+ selection

using a CellPro (Bothell, WA) avidin column. Either freshly isolated or cryopreserved CD34+ cell enriched fractions are used for the assay. Duplicate cultures for each serial dilution of sample (concentration range from 1 pM to 1204 pM) are prepared with 1x104 cells in 1ml of 0.9% methycellulose containing medium without additional growth factors (Methocult H4230 from Stem Cell Technologies, Vancouver, BC.). In some experiments, Methocult H4330 containing erythropoietin (EPO) was used instead of Methocult H4230, or Stem Cell Factor (SCF), 50 ng/mL (Biosource International, Camarillo, CA) was added. After culturing for 7-9 days, colonies containing >30 cells are counted. In order to rule out subjective bias in scoring, assays are scored blind.

Additional details about recombinant DNA methods which may be used to create the variants, express them in bacteria, mammalian cells or insect cells, purification and refold of the desired proteins and assays for determining the bioactivity of the proteins may be found in co-filed Applications WO 95/00646, WO 94/12639, WO 94/12638, WO 95/20976, WO 95/21197, WO 95/20977, WO 95/21254 and US 08/383,035 which are hereby incorporated by reference in their entirety.

Further details known to those skilled in the art may be found in T. Maniatis, et al., Molecular Cloning, A Laboratory

Manual, Cold Spring Harbor Laboratory, 1982) and references cited therein, incorporated herein by reference; and in J. Sambrook, et al., Molecular Cloning, A Laboratory Manual, 2nd edition, Cold Spring Harbor Laboratory, 1989) and references cited therein, are incorporated herein by reference.

TABLE 1
OLIGONUCLEOTIDES

c-mplNcoI
ACGTCCATGGCNTCNCCNGCNCCNCCTGCTTGTGCACTCCGAGTC
(SEQ ID NO:13)
N=A,C,G or T

Ecompl	ATGCACGAATTCCCTGACGCAGAGGGTGGA (SEQ ID NO:14)
c-mplHindIII	TGACAAGCTTACCTGACGCAGAGGGTGGACCCT (SEQ ID NO:15)
4L-5′	AATTCGGCAA (SEQ ID NO:16)
4L-3′	CATGTTGCCG (SEQ ID NO:17)
5L-5′	AATTCGGCGGCAA (SEQ ID NO:18)
5L-3′	CATGTTGCCGCCG (SEQ ID NO:19)
8L-5′	AATTCGGCGGCAACGGCGGCAA (SEQ ID NO:20)
8L-3′	CATGTTGCCGCCGTTGCCGCCG (SEQ ID NO:21)
31-5′	CGATCCATGGAGGTTCACCCTTTGCCT (SEQ ID NO:22)
31-3′	GATCAAGCTTATGGGCACTGGCTCAGTCT (SEQ ID NO:23)
35-5′	CGATACATGTTGCCTACACCTGTCCTG (SEQ ID NO:24)
35-3′	GATCAAGCTTAAGGGTGAACCTCTGGGCA (SEQ ID NO:25)
39-5′	CGATCCATGGTCCTGCTGCCTGCTGTG (SEQ ID NO:26)
39-3′	GATCAAGCTTAAGGTGTAGGCAAAGGGTG (SEQ ID NO:27)
43-5′	CGATCCATGGCTGTGGACTTTAGCTTGGGA (SEQ ID NO:28)
43-3′	GATCAAGCTTAAGGCAGCAGGACAGGTGT (SEQ ID NO:29)
45-5′	CGATCCATGGACTTTAGCTTGGGAGAA (SEQ ID NO:30)
45-3′	GATCAAGCTTACACAGCAGGCAGCAGGAC (SEQ ID NO:31)
49-5′	CGATCCATGGGAGAATGGAAAACCCAG (SEQ ID NO:32)

49-3′	GATCAAGCTTACAAGCTAAAGTCCACAGC (SEQ ID NO:33)
82-5′	CGATCCATGGGACCCACTTGCCTCTCA (SEQ ID NO:34)
82-3′	GATCAAGCTTACAGTTGTCCCCGTGCTGC (SEQ ID NO:35)
109-5′	CAGTCCATGGGAACCCAGCTTCCTCCA (SEQ ID NO:36)
109-3′	GATCAAGCTTAAAGGAGGCTCTGCAGGGC (SEQ ID NO:37)
116-5′	CGATCCATGGGCAGGACCACAGCTCAC (SEQ ID NO:38)
116-3′	GATCAAGCTTACTGTGGAGGAAGCTGGGTT (SEQ ID NO:39)
120-5′	CGATCCATGGCTCACAAGGATCCCAATGCC (SEQ ID NO:40)
120-3′	GATCAAGCTTATGTGGTCCTGCCCTGTGG (SEQ ID NO:41)
123-5′	CGATCCATGGATCCCAATGCCATCTTCCTG (SEQ ID NO:42)
123-3′	GATCAAGCTTACTTGTGAGCTGTGGTCCT (SEQ ID NO:43)
126-5′	CGATCCATGGCCATCTTCCTGAGCTTCCAA (SEQ ID NO:44)
126-3′	GATCAAGCTTAATTGGGATCCTTGTGAGCTGT (SEQ ID NO:45)
SYNNOXA1.REQ	AATTCCGTCG TAAACTGACC TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAGT ACGTAGAGGG CGGTGGAGGC TCC (SEQ ID NO:46)
SYNNOXA2.REQ	CCGGGGAGCC TCCACCGCCC TCTACGTACT GTTGAGCCTG CGCGTTCTCC AAGGTTTTCA GATAGAAGGT CAGTTTACGA CGG (SEQ ID NO:47)
L1syn.for	GTTACCCTTG AGCAAGCGCA GGAACAACAG GGTGGTGGCT CTAACTGCTC TATAATGAT (SEQ ID NO:48)
L1syn.rev	CGATCATTAT AGAGCAGTTA GAGCCACCAC CCTGTTGTTC CTGCGCTTGC TCAAGG (SEQ ID NO:49)
L3syn.for	GTTACCCTTG AGCAAGCGCA GGAACAACAG GGTGGTGGCT CTGGCGGTGG CAGCGGCGGC GGTTCTAACT GCTCTATAAT GAT (SEQ ID NO:50)

L3syn.rev	CGATCATTAT AGAGCAGTTA GAACCGCCGC CGCTGCCACC GCCAGAGCCA CCACCCTGTT GTTCCTGCGC TTGCTCAAGG (SEQ ID NO:51)
35start.seq	GATCGACCAT GGCTCTGGAC CCGAACAACC TC (SEQ ID NO:52)
34rev.seq	CTCGATTACG TACAAAGGTG CAGGTGGT (SEQ ID NO:53)
70start.seq	GATCGACCAT GGCTAATGCA TCAGGTATTG AG (SEQ ID NO:54)
69rev.seq	CTCGATTACG TATTCTAAGT TCTTGACA (SEQ ID NO:55)
91start.seq	GATCGACCAT GGCTGCACCC TCTCGACATC CA (SEQ ID NO:56)
90rev.seq	CTCGATTACG TAGGCCGTGG CAGAGGGC (SEQ ID NO:57)
101start.seq	GATCGACCAT GGCTGCAGGT GACTGGCAAG AA (SEQ ID NO:58)
100rev.seq	CTCGATTACG TACTTGATGA TGATTGGA (SEQ ID NO:59)
L-11start.seq	GCTCTGAGAG CCGCCAGAGC CGCCAGAGGG CTGCGCAAGG TGGCGTAGAA CGCG (SEQ ID NO:60)
L-11stop.seq	CAGCCCTCTG GCGGCTCTGG CGGCTCTCAG AGCTTCCTGC TCAAGTCTTT AGAG (SEQ ID NO:61)
P-blstart.seq	GGGCTGCGCA AGGTGGCG (SEQ ID NO:62)
P-blstop.seq	ACACCATTGG GCCCTGCCAG C (SEQ ID NO:63)
39start.seq	GATCGACCAT GGCTTACAAG CTGTGCCACC CC (SEQ ID NO:64)
38stop.Seq	CGATCGAAGC TTATTAGGTG GCACACAGCT TCTCCT (SEQ ID NO:65)
97start.seq	GATCGACCAT GGCTCCCGAG TTGGGTCCCA CC (SEQ ID NO:66)
96stop.Seq	CGATCGAAGC TTATTAGGAT ATCCCTTCCA GGGCCT (SEQ ID NO:67)
126start.seq	GATCGACCAT GGCTATGGCC CCTGCCCTGC AG

(SEQ ID NO:68)

125stop.Seq CGATCGAAGC TTATTATCCC AGTTCTTCCA TCTGCT
(SEQ ID NO:69)

133start.seq GATCGACCAT GGCTACCCAG GGTGCCATGC CG
(SEQ ID NO:70)

132stop.seq CGATCGAAGC TTATTAGGGC TGCAGGGCAG GGGCCA
(SEQ ID NO:71)

142start.seq GATCGACCAT GGCTTCTGCT TTCCAGCGCC GG
(SEQ ID NO:72)

141stop.Seq CGATCGAAGC TTATTAGGCG AAGGCCGGCA TGGCAC
(SEQ ID NO:73)

GLYXA1 GTAGAGGGCG GTGGAGGCTC C (SEQ ID NO:74)

GLYXA2 CCGGGGAGCC TCCACCGCCC TCTAC (SEQ ID NO:75)

1GGGSfor TTCTACGCCA CCTTGCGCAG CCCGGCGGCG GCTCTGACAT GTCTACACCA TTG (SEQ ID NO:76)

1GGGSrev CAATGGTGTA GACATGTCAG AGCCGCCGCC GGGCTGCGCA AGGTGGCGTA GAA (SEQ ID NO:77)

Synnoxa1.req AATTCCGTCG TAAACTGACC TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAGT ACGTAGAGGG CGGTGGAGGC TCC (SEQ ID NO:240)

Synnoxa2.req CCGGGGAGCC TCCACCGCCC TCTACGTACT GTTGAGCCTG CGCGTTCTCC AAGGTTTTCA GATAGAAGGT CAGTTTACGA CGG (SEQ ID NO:241)

TABLE 2
GENE SEQUENCES

pMON30304

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
CATGT (SEQ ID NO:78)

pMON26458

TCCCCAGCTCCACCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGT
CCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGC
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CACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCC
TGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCC
AATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGT
AGGAGGGTCCACCCTCTGCGTCAGGGAATTC (SEQ ID NO:79)

pMON28548

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CCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGC
CTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGAC
ATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACC
CACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCC
TGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCC
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CTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCACAGCAGACTG
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CCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCC
CTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGAGCCTCCTTGG
AACCCAGGGCAGGACCACAGCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACC
TGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGG
(SEQ ID NO:80)

pMON28500

TCCCCAGCTCCACCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGT
CCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGC
CTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGAC
ATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACC
CACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCC
TGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCC
AATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGT
AGGAGGGTCCACCCTCTGCGTCAGGGAATTCGGCAACATGGCGTCTCCCGCTCCGCCTGCTT
GTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCACAGCAGACTGAGC
CAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGCCTGCTGTGGACTTTAGCTT
GGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTGACCC
TTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCCCTC
CTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGAGCCTCCTTGGAAC

CCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCCAATGCCATCTTCCTGAGCT
TCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGC
GTCAGG (SEQ ID NO:81)

pMON28501

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CCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGC
CTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGAC
ATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACC
CACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCC
TGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCC
AATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGT
AGGAGGGTCCACCCTCTGCGTCAGGGAATTCGGCGGCAACATGGCGTCTCCCGCTCCGCCTG
CTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCACAGCAGACTG
AGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGCCTGCTGTGGACTTTAG
CTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTGA
CCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCC
CTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGAGCCTCCTTGG
AACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCCAATGCCATCTTCCTGA
GCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGTAGGAGGGTCCACCCTC
TGCGTCAGG (SEQ ID NO:82)

pMON28502

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CCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGC
CTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGAC
ATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACC
CACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCC
TGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCC
AATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGT
AGGAGGGTCCACCCTCTGCGTCAGGGAATTCGGCGGCAACGGCGGCAACATGGCGTCCCCAG
CGCCGCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCAC
AGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGCCTGCTGT
GGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTGG
GAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACCCACTTGC
CTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGAG
CCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCCAATGCCA
TCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGTAGGAGGG
TCCACCCTCTGCGTCAGG (SEQ ID NO:83)

Syntan1

CATGGCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCAC
CTTTGCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTT

CGACTTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTAT
TGAGGCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGAC
ATCCAATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTG
GTTACCCTTGAGCAAGCGCAGGAACAACAGGGTGGTGGCTCTAACTGCTCTATAATGATCGA
TGAAATTATACATCACTTAAAGAGACCACCTGCACCTTTGCTGGACCCGAACAACCTCAATG
ACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGACTTCCAAACCTGGAGAGCTTCGTA
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ATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCCAATCATCATCAAGGCAGGTGACT
GGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTACCCTTGAGCAAGCGCAGGAACAA
CAGTAC (SEQ ID NO:84)

Syntan3

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   1  CATGGCTAAC TGCTCTATAA TGATCGATGA AATTATACAT CACTTAAAGA
  51  GACCACCTGC ACCTTTGCTG GACCCGAACA ACCTCAATGA CGAAGACGTC
 101  TCTATCCTGA TGGACCGAAA CCTTCGACTT CCAAACCTGG AGAGCTTCGT
 151  AAGGGCTGTC AAGAACTTAG AAAATGCATC AGGTATTGAG GCAATTCTTC
 201  GTAATCTCCA ACCATGTCTG CCCTCTGCCA CGGCCGCACC CTCTCGACAT
 251  CCAATCATCA TCAAGGCAGG TGACTGGCAA GAATTCCGGG AAAAACTGAC
 301  GTTCTATCTG GTTACCCTTG AGCAAGCGCA GGAACAACAG GGTGGTGGCT
 351  CTGGCGGTGG CAGCGGCGGC GGTTCTAACT GCTCTATAAT GATCGATGAA
 401  ATTATACATC ACTTAAAGAG ACCACCTGCA CCTTTGCTGG ACCCGAACAA
 451  CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC CTTCGACTTC
 501  CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA
 551  GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC
 601  GGCCGCACCC TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG
 651  AATTCCGGGA AAAACTGACG TTCTATCTGG TTACCCTTGA GCAAGCGCAG
 701  GAACAACAGT AC (SEQ ID NO:85)
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pMON31104

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   1  ATGGCTCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT
  51  GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA
 101  AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG TAATCTCCAA
 151  CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC CAATCATCAT
 201  CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG TTCTATCTGG
 251  TTACCCTTGA GCAAGCGCAG GAACAACAGG GTGGTGGCTC TAACTGCTCT
 301  ATAATGATCG ATGAAATTAT ACATCACTTA AAGAGACCAC CTGCACCTTT
 351  GTACGTAGAG GGCGGTGGAG GCTCCCCGGG TGAACCGTCT GGTCCAATCT
 401  CTACTATCAA CCCGTCTCCT CCGTCTAAAG AATCTCATAA ATCTCCAAAC
 451  ATGGCTACCC AGGGTGCCAT GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG
 501  GGCAGGAGGG GTCCTGGTTG CTAGCCATCT GCAGAGCTTC CTGGAGGTGT
 551  CGTACCGCGT TCTACGCCAC CTTGCGCAGC CCTCTGGCGG CTCTGGCGGC
 601  TCTCAGAGCT TCCTGCTCAA GTCTTTAGAG CAAGTGAGAA AGATCCAGGG
 651  CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC AAGCTGTGCC
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 701  ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT
 751  CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG
 801  CCAACTCCAT AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG
 851  AAGGGATATC CCCCGAGTTG GGTCCCACCT TGGACACACT GCAGCTGGAC
 901  GTCGCCGACT TTGCCACCAC CATCTGGCAG CAGATGGAAG AACTGGGAAT
 951  GGCCCCTGCC CTGCAGCCCT AATAA (SEQ ID NO:86)
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pMON31105

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   1  ATGGCTAATG CATCAGGTAT TGAGGCAATT CTTCGTAATC TCCAACCATG
  51  TCTGCCCTCT GCCACGGCCG CACCCTCTCG ACATCCAATC ATCATCAAGG
 101  CAGGTGACTG GCAAGAATTC CGGGAAAAAC TGACGTTCTA TCTGGTTACC
 151  CTTGAGCAAG CGCAGGAACA ACAGGGTGGT GGCTCTAACT GCTCTATAAT
 201  GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA CCTTTGCTGG
 251  ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC
 301  CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA
 351  ATACGTAGAG GGCGGTGGAG GCTCCCCGGG TGAACCGTCT GGTCCAATCT
 401  CTACTATCAA CCCGTCTCCT CCGTCTAAAG AATCTCATAA ATCTCCAAAC
 451  ATGGCTACCC AGGGTGCCAT GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG
 501  GGCAGGAGGG GTCCTGGTTG CTAGCCATCT GCAGAGCTTC CTGGAGGTGT
 551  CGTACCGCGT TCTACGCCAC CTTGCGCAGC CCTCTGGCGG CTCTGGCGGC
 601  TCTCAGAGCT TCCTGCTCAA GTCTTTAGAG CAAGTGAGAA AGATCCAGGG
 651  CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC AAGCTGTGCC
 701  ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT
 751  CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG
 801  CCAACTCCAT AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG
 851  AAGGGATATC CCCCGAGTTG GGTCCCACCT TGGACACACT GCAGCTGGAC
 901  GTCGCCGACT TTGCCACCAC CATCTGGCAG CAGATGGAAG AACTGGGAAT
 951  GGCCCCTGCC CTGCAGCCCT AATAA (SEQ ID NO:87)
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pMON31106

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  51  AGAATTCCGG GAAAAACTGA CGTTCTATCT GGTTACCCTT GAGCAAGCGC
 101  AGGAACAACA GGGTGGTGGC TCTAACTGCT CTATAATGAT CGATGAAATT
 151  ATACATCACT TAAAGAGACC ACCTGCACCT TTGCTGGACC CGAACAACCT
 201  CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT CGACTTCCAA
 251  ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT
 301  ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC
 351  CTACGTAGAG GGCGGTGGAG GCTCCCCGGG TGAACCGTCT GGTCCAATCT
 401  CTACTATCAA CCCGTCTCCT CCGTCTAAAG AATCTCATAA ATCTCCAAAC
 451  ATGGCTACCC AGGGTGCCAT GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG
 501  GGCAGGAGGG GTCCTGGTTG CTAGCCATCT GCAGAGCTTC CTGGAGGTGT
 551  CGTACCGCGT TCTACGCCAC CTTGCGCAGC CCTCTGGCGG CTCTGGCGGC
 601  TCTCAGAGCT TCCTGCTCAA GTCTTTAGAG CAAGTGAGAA AGATCCAGGG
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 651  CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC AAGCTGTGCC
 701  ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT
 751  CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG
 801  CCAACTCCAT AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG
 851  AAGGGATATC CCCCGAGTTG GGTCCCACCT TGGACACACT GCAGCTGGAC
 901  GTCGCCGACT TTGCCACCAC CATCTGGCAG CAGATGGAAG AACTGGGAAT
 951  GGCCCCTGCC CTGCAGCCCT AATAA (SEQ ID NO:88)
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pMON31107

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  51  GGTTACCCTT GAGCAAGCGC AGGAACAACA GGGTGGTGGC TCTAACTGCT
 101  CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT
 151  TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA
 201  CCGAAACCTT CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA
 251  ACTTAGAAAA TGCATCAGGT ATTGAGGCAA TTCTTCGTAA TCTCCAACCA
 301  TGTCTGCCCT CTGCCACGGC CGCACCCTCT CGACATCCAA TCATCATCAA
 351  GTACGTAGAG GGCGGTGGAG GCTCCCCGGG TGAACCGTCT GGTCCAATCT
 401  CTACTATCAA CCCGTCTCCT CCGTCTAAAG AATCTCATAA ATCTCCAAAC
 451  ATGGCTACCC AGGGTGCCAT GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG
 501  GGCAGGAGGG GTCCTGGTTG CTAGCCATCT GCAGAGCTTC CTGGAGGTGT
 551  CGTACCGCGT TCTACGCCAC CTTGCGCAGC CCTCTGGCGG CTCTGGCGGC
 601  TCTCAGAGCT TCCTGCTCAA GTCTTTAGAG CAAGTGAGAA AGATCCAGGG
 651  CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC AAGCTGTGCC
 701  ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT
 751  CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG
 801  CCAACTCCAT AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG
 851  AAGGGATATC CCCCGAGTTG GGTCCCACCT TGGACACACT GCAGCTGGAC
 901  GTCGCCGACT TTGCCACCAC CATCTGGCAG CAGATGGAAG AACTGGGAAT
 951  GGCCCCTGCC CTGCAGCCCT AATAA (SEQ ID NO:89)
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pMON31108

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  51  GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA
 101  AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG TAATCTCCAA
 151  CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC CAATCATCAT
 201  CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG TTCTATCTGG
 251  TTACCCTTGA GCAAGCGCAG GAACAACAGG GTGGTGGCTC TGGCGGTGGC
 301  AGCGGCGGCG GTTCTAACTG CTCTATAATG ATCGATGAAA TTATACATCA
 351  CTTAAAGAGA CCACCTGCAC CTTTGTACGT AGAGGGCGGT GGAGGCTCCC
 401  CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT
 451  AAAGAATCTC ATAAATCTCC AAACATGGCT ACCCAGGGTG CCATGCCGGC
 501  CTTCGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG GTTGCTAGCC
 551  ATCTGCAGAG CTTCCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG
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 601  CAGCCCTCTG GCGGCTCTGG CGGCTCTCAG AGCTTCCTGC TCAAGTCTTT
 651  AGAGCAAGTG AGAAAGATCC AGGGCGATGG CGCAGCGCTC CAGGAGAAGC
 701  TGTGTGCCAC CTACAAGCTG TGCCACCCCG AGGAGCTGGT GCTGCTCGGA
 751  CACTCTCTGG GCATCCCCTG GGCTCCCCTG AGCTCCTGCC CCAGCCAGGC
 801  CCTGCAGCTG GCAGGCTGCT TGAGCCAACT CCATAGCGGC CTTTTCCTCT
 851  ACCAGGGGCT CCTGCAGGCC CTGGAAGGGA TATCCCCCGA GTTGGGTCCC
 901  ACCTTGGACA CACTGCAGCT GGACGTCGCC GACTTTGCCA CCACCATCTG
 951  GCAGCAGATG GAAGAACTGG GAATGGCCCC TGCCCTGCAG CCCTAATAA
     (SEQ ID NO:90)
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pMON31109

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   1  ATGGCTAATG CATCAGGTAT TGAGGCAATT CTTCGTAATC TCCAACCATG
  51  TCTGCCCTCT GCCACGGCCG CACCCTCTCG ACATCCAATC ATCATCAAGG
 101  CAGGTGACTG GCAAGAATTC CGGGAAAAAC TGACGTTCTA TCTGGTTACC
 151  CTTGAGCAAG CGCAGGAACA ACAGGGTGGT GGCTCTGGCG GTGGCAGCGG
 201  CGGCGGTTCT AACTGCTCTA TAATGATCGA TGAAATTATA CATCACTTAA
 251  AGAGACCACC TGCACCTTTG CTGGACCCGA ACAACCTCAA TGACGAAGAC
 301  GTCTCTATCC TGATGGACCG AAACCTTCGA CTTCCAAACC TGGAGAGCTT
 351  CGTAAGGGCT GTCAAGAACT TAGAATACGT AGAGGGCGGT GGAGGCTCCC
 401  CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT
 451  AAAGAATCTC ATAAATCTCC AAACATGGCT ACCCAGGGTG CCATGCCGGC
 501  CTTCGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG GTTGCTAGCC
 551  ATCTGCAGAG CTTCCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG
 601  CAGCCCTCTG GCGGCTCTGG CGGCTCTCAG AGCTTCCTGC TCAAGTCTTT
 651  AGAGCAAGTG AGAAAGATCC AGGGCGATGG CGCAGCGCTC CAGGAGAAGC
 701  TGTGTGCCAC CTACAAGCTG TGCCACCCCG AGGAGCTGGT GCTGCTCGGA
 751  CACTCTCTGG GCATCCCCTG GGCTCCCCTG AGCTCCTGCC CCAGCCAGGC
 801  CCTGCAGCTG GCAGGCTGCT TGAGCCAACT CCATAGCGGC CTTTTCCTCT
 851  ACCAGGGGCT CCTGCAGGCC CTGGAAGGGA TATCCCCCGA GTTGGGTCCC
 901  ACCTTGGACA CACTGCAGCT GGACGTCGCC GACTTTGCCA CCACCATCTG
 951  GCAGCAGATG GAAGAACTGG GAATGGCCCC TGCCCTGCAG CCCTAATAA
     (SEQ ID NO:91)
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pMON31110

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  51  AGAATTCCGG GAAAAACTGA CGTTCTATCT GGTTACCCTT GAGCAAGCGC
 101  AGGAACAACA GGGTGGTGGC TCTGGCGGTG GCAGCGGCGG CGGTTCTAAC
 151  TGCTCTATAA TGATCGATGA AATTATACAT CACTTAAAGA GACCACCTGC
 201  ACCTTTGCTG GACCCGAACA ACCTCAATGA CGAAGACGTC TCTATCCTGA
 251  TGGACCGAAA CCTTCGACTT CCAAACCTGG AGAGCTTCGT AAGGGCTGTC
 301  AAGAACTTAG AAAATGCATC AGGTATTGAG GCAATTCTTC GTAATCTCCA
 351  ACCATGTCTG CCCTCTGCCA CGGCCTACGT AGAGGGCGGT GGAGGCTCCC
 401  CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT
 451  AAAGAATCTC ATAAATCTCC AAACATGGCT ACCCAGGGTG CCATGCCGGC
 501  CTTCGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG GTTGCTAGCC
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 551  ATCTGCAGAG CTTCCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG
 601  CAGCCCTCTG GCGGCTCTGG CGGCTCTCAG AGCTTCCTGC TCAAGTCTTT
 651  AGAGCAAGTG AGAAAGATCC AGGGCGATGG CGCAGCGCTC CAGGAGAAGC
 701  TGTGTGCCAC CTACAAGCTG TGCCACCCCG AGGAGCTGGT GCTGCTCGGA
 751  CACTCTCTGG GCATCCCCTG GGCTCCCCTG AGCTCCTGCC CCAGCCAGGC
 801  CCTGCAGCTG GCAGGCTGCT TGAGCCAACT CCATAGCGGC CTTTTCCTCT
 851  ACCAGGGGCT CCTGCAGGCC CTGGAAGGGA TATCCCCCGA GTTGGGTCCC
 901  ACCTTGGACA CACTGCAGCT GGACGTCGCC GACTTTGCCA CCACCATCTG
 951  GCAGCAGATG GAAGAACTGG GAATGGCCCC TGCCCTGCAG CCCTAATAA
      (SEQ ID NO:92)
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pMON31111

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   1  ATGGCTGCAG GTGACTGGCA AGAATTCCGG GAAAAACTGA CGTTCTATCT
  51  GGTTACCCTT GAGCAAGCGC AGGAACAACA GGGTGGTGGC TCTGGCGGTG
 101  GCAGCGGCGG CGGTTCTAAC TGCTCTATAA TGATCGATGA AATTATACAT
 151  CACTTAAAGA GACCACCTGC ACCTTTGCTG GACCCGAACA ACCTCAATGA
 201  CGAAGACGTC TCTATCCTGA TGGACCGAAA CCTTCGACTT CCAAACCTGG
 251  AGAGCTTCGT AAGGGCTGTC AAGAACTTAG AAAATGCATC AGGTATTGAG
 301  GCAATTCTTC GTAATCTCCA ACCATGTCTG CCCTCTGCCA CGGCCGCACC
 351  CTCTCGACAT CCAATCATCA TCAAGTACGT AGAGGGCGGT GGAGGCTCCC
 401  CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT
 451  AAAGAATCTC ATAAATCTCC AAACATGGCT ACCCAGGGTG CCATGCCGGC
 501  CTTCGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG GTTGCTAGCC
 551  ATCTGCAGAG CTTCCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG
 601  CAGCCCTCTG GCGGCTCTGG CGGCTCTCAG AGCTTCCTGC TCAAGTCTTT
 651  AGAGCAAGTG AGAAAGATCC AGGGCGATGG CGCAGCGCTC CAGGAGAAGC
 701  TGTGTGCCAC CTACAAGCTG TGCCACCCCG AGGAGCTGGT GCTGCTCGGA
 751  CACTCTCTGG GCATCCCCTG GGCTCCCCTG AGCTCCTGCC CCAGCCAGGC
 801  CCTGCAGCTG GCAGGCTGCT TGAGCCAACT CCATAGCGGC CTTTTCCTCT
 851  ACCAGGGGCT CCTGCAGGCC CTGGAAGGGA TATCCCCCGA GTTGGGTCCC
 901  ACCTTGGACA CACTGCAGCT GGACGTCGCC GACTTTGCCA CCACCATCTG
 951  GCAGCAGATG GAAGAACTGG GAATGGCCCC TGCCCTGCAG CCCTAATAA
      (SEQ ID NO:93)
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pMON13182

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   1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
  51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 101  CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
 151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 351  CGGTGGAGGC TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTT
 401  ACAAGCTGTG CCACCCCGAG GAGCTGGTGC TGCTCGGACA CTCTCTGGGC
 451  ATCCCCTGGG CTCCCCTGAG CTCCTGCCCC AGCCAGGCCC TGCAGCTGGC
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 501  AGGCTGCTTG AGCCAACTCC ATAGCGGCCT TTTCCTCTAC CAGGGGCTCC
 551  TGCAGGCCCT GGAAGGGATA TCCCCCGAGT TGGGTCCCAC CTTGGACACA
 601  CTGCAGCTGG ACGTCGCCGA CTTTGCCACC ACCATCTGGC AGCAGATGGA
 651  AGAACTGGGA ATGGCCCCTG CCCTGCAGCC CACCCAGGGT GCCATGCCGG
 701  CCTTCGCCTC TGCTTTCCAG CGCCGGGCAG GAGGGGTCCT GGTTGCTAGC
 751  CATCTGCAGA GCTTCCTGGA GGTGTCGTAC CGCGTTCTAC GCCACCTTGC
 801  GCAGCCCTCT GGCGGCTCTG GCGGCTCTCA GAGCTTCCTG CTCAAGTCTT
 851  TAGAGCAAGT GAGAAAGATC CAGGGCGATG GCGCAGCGCT CCAGGAGAAG
 901  CTGTGTGCCA CCTAATAA (SEQ ID NO:94)
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pMON13183

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   1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
  51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 101  CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
 151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
 401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTTACAAG
 451  CTGTGCCACC CCGAGGAGCT GGTGCTGCTC GGACACTCTC TGGGCATCCC
 501  CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG CTGGCAGGCT
 551  GCTTGAGCCA ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG
 601  GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA
 651  GCTGGACGTC GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC
 701  TGGGAATGGC CCCTGCCCTG CAGCCCACCC AGGGTGCCAT GCCGGCCTTC
 751  GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG GTCCTGGTTG CTAGCCATCT
 801  GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC CTTGCGCAGC
 851  CCTCTGGCGG CTCTGGCGGC TCTCAGAGCT TCCTGCTCAA GTCTTTAGAG
 901  CAAGTGAGAA AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG
 951  TGCCACCTAA TAA (SEQ ID NO:95)
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pMON13184

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   1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
  51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 101  CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
 151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 351  CGGTGGAGGC TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTC
 401  CCGAGTTGGG TCCCACCTTG GACACACTGC AGCTGGACGT CGCCGACTTT
 451  GCCACCACCA TCTGGCAGCA GATGGAAGAA CTGGGAATGG CCCCTGCCCT
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 501  GCAGCCCACC CAGGGTGCCA TGCCGGCCTT CGCCTCTGCT TTCCAGCGCC
 551  GGGCAGGAGG GGTCCTGGTT GCTAGCCATC TGCAGAGCTT CCTGGAGGTG
 601  TCGTACCGCG TTCTACGCCA CCTTGCGCAG CCCTCTGGCG GCTCTGGCGG
 651  CTCTCAGAGC TTCCTGCTCA AGTCTTTAGA GCAAGTGAGA AAGATCCAGG
 701  GCGATGGCGC AGCGCTCCAG GAGAAGCTGT GTGCCACCTA CAAGCTGTGC
 751  CACCCCGAGG AGCTGGTGCT GCTCGGACAC TCTCTGGGCA TCCCCTGGGC
 801  TCCCCTGAGC TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA GGCTGCTTGA
 851  GCCAACTCCA TAGCGGCCTT TTCCTCTACC AGGGGCTCCT GCAGGCCCTG
 901  GAAGGGATAT CCTAATAA (SEQ ID NO:96)
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pMON13185

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   1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
  51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 101  CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
 151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
 401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTCCCGAG
 451  TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC
 501  CACCATCTGG CAGCAGATGG AAGAACTGGG AATGGCCCCT GCCCTGCAGC
 551  CCACCCAGGG TGCCATGCCG GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA
 601  GGAGGGGTCC TGGTTGCTAG CCATCTGCAG AGCTTCCTGG AGGTGTCGTA
 651  CCGCGTTCTA CGCCACCTTG CGCAGCCCTC TGGCGGCTCT GGCGGCTCTC
 701  AGAGCTTCCT GCTCAAGTCT TTAGAGCAAG TGAGAAAGAT CCAGGGCGAT
 751  GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC ACCTACAAGC TGTGCCACCC
 801  CGAGGAGCTG GTGCTGCTCG GACACTCTCT GGGCATCCCC TGGGCTCCCC
 851  TGAGCTCCTG CCCCAGCCAG GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA
 901  CTCCATAGCG GCCTTTTCCT CTACCAGGGG CTCCTGCAGG CCCTGGAAGG
 951  GATATCCTAA TAA (SEQ ID NO:97)
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pMON13186

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   1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
  51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 101  CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
 151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 351  CGGTGGAGGC TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA
 401  TGGCCCCTGC CCTGCAGCCC ACCCAGGGTG CCATGCCGGC CTTCGCCTCT
 451  GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG GTTGCTAGCC ATCTGCAGAG
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 501  CTTCCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG CAGCCCTCTG
 551  GCGGCTCTGG CGGCTCTCAG AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG
 601  AGAAAGATCC AGGGCGATGG CGCAGCGCTC CAGGAGAAGC TGTGTGCCAC
 651  CTACAAGCTG TGCCACCCCG AGGAGCTGGT GCTGCTCGGA CACTCTCTGG
 701  GCATCCCCTG GGCTCCCCTG AGCTCCTGCC CCAGCCAGGC CCTGCAGCTG
 751  GCAGGCTGCT TGAGCCAACT CCATAGCGGC CTTTTCCTCT ACCAGGGGCT
 801  CCTGCAGGCC CTGGAAGGGA TATCCCCCGA GTTGGGTCCC ACCTTGGACA
 851  CACTGCAGCT GGACGTCGCC GACTTTGCCA CCACCATCTG GCAGCAGATG
 901  GAAGAACTGG GATAATAA (SEQ ID NO:98)
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pMON13187

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   1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
  51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 101  CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
 151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
 401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTATGGCC
 451  CCTGCCCTGC AGCCCACCCA GGGTGCCATG CCGGCCTTCG CCTCTGCTTT
 501  CCAGCGCCGG GCAGGAGGGG TCCTGGTTGC TAGCCATCTG CAGAGCTTCC
 551  TGGAGGTGTC GTACCGCGTT CTACGCCACC TTGCGCAGCC CTCTGGCGGC
 601  TCTGGCGGCT CTCAGAGCTT CCTGCTCAAG TCTTTAGAGC AAGTGAGAAA
 651  GATCCAGGGC GATGGCGCAG CGCTCCAGGA GAAGCTGTGT GCCACCTACA
 701  AGCTGTGCCA CCCCGAGGAG CTGGTGCTGC TCGGACACTC TCTGGGCATC
 751  CCCTGGGCTC CCCTGAGCTC CTGCCCCAGC CAGGCCCTGC AGCTGGCAGG
 801  CTGCTTGAGC CAACTCCATA GCGGCCTTTT CCTCTACCAG GGGCTCCTGC
 851  AGGCCCTGGA AGGGATATCC CCCGAGTTGG GTCCCACCTT GGACACACTG
 901  CAGCTGGACG TCGCCGACTT TGCCACCACC ATCTGGCAGC AGATGGAAGA
 951  ACTGGGATAA TAA (SEQ ID NO:99)
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pMON13188

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   1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
  51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 101  CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
 151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 351  CGGTGGAGGC TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA
 401  CCCAGGGTGC CATGCCGGCC TTCGCCTCTG CTTTCCAGCG CCGGGCAGGA
 451  GGGGTCCTGG TTGCTAGCCA TCTGCAGAGC TTCCTGGAGG TGTCGTACCG
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 501  CGTTCTACGC CACCTTGCGC AGCCCTCTGG CGGCTCTGGC GGCTCTCAGA
 551  GCTTCCTGCT CAAGTCTTTA GAGCAAGTGA GAAAGATCCA GGGCGATGGC
 601  GCAGCGCTCC AGGAGAAGCT GTGTGCCACC TACAAGCTGT GCCACCCCGA
 651  GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG GCTCCCCTGA
 701  GCTCCTGCCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC
 751  CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCCC TGGAAGGGAT
 801  ATCCCCCGAG TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG
 851  ACTTTGCCAC CACCATCTGG CAGCAGATGG AAGAACTGGG AATGGCCCCT
 901  GCCCTGCAGC CCTAATAA (SEQ ID NO:100)
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pMON13189

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   1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
  51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 101  CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
 151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
 401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTACCCAG
 451  GGTGCCATGC CGGCCTTCGC CTCTGCTTTC CAGCGCCGGG CAGGAGGGGT
 501  CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG TACCGCGTTC
 551  TACGCCACCT TGCGCAGCCC TCTGGCGGCT CTGGCGGCTC TCAGAGCTTC
 601  CTGCTCAAGT CTTTAGAGCA AGTGAGAAAG ATCCAGGGCG ATGGCGCAGC
 651  GCTCCAGGAG AAGCTGTGTG CCACCTACAA GCTGTGCCAC CCCGAGGAGC
 701  TGGTGCTGCT CGGACACTCT CTGGGCATCC CCTGGGCTCC CCTGAGCTCC
 751  TGCCCCAGCC AGGCCCTGCA GCTGGCAGGC TGCTTGAGCC AACTCCATAG
 801  CGGCCTTTTC CTCTACCAGG GGCTCCTGCA GGCCCTGGAA GGGATATCCC
 851  CCGAGTTGGG TCCCACCTTG GACACACTGC AGCTGGACGT CGCCGACTTT
 901  GCCACCACCA TCTGGCAGCA GATGGAAGAA CTGGGAATGG CCCCTGCCCT
 951  GCAGCCCTAA TAA (SEQ ID NO:101)
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pMON13190

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   1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
  51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 101  CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
 151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 351  CGGTGGAGGC TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTT
 401  CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG
 451  AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTC
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 501  TGGCGGCTCT GGCGGCTCTC AGAGCTTCCT GCTCAAGTCT TTAGAGCAAG
 551  TGAGAAAGAT CCAGGGCGAT GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC
 601  ACCTACAAGC TGTGCCACCC CGAGGAGCTG GTGCTGCTCG GACACTCTCT
 651  GGGCATCCCC TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG GCCCTGCAGC
 701  TGGCAGGCTG CTTGAGCCAA CTCCATAGCG GCCTTTTCCT CTACCAGGGG
 751  CTCCTGCAGG CCCTGGAAGG GATATCCCCC GAGTTGGGTC CCACCTTGGA
 801  CACACTGCAG CTGGACGTCG CCGACTTTGC CACCACCATC TGGCAGCAGA
 851  TGGAAGAACT GGGAATGGCC CCTGCCCTGC AGCCCACCCA GGGTGCCATG
 901  CCGGCCTTCG CCTAATAA (SEQ ID NO:102)
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pMON13191

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   1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
  51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 101  CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
 151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
 401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTTCTGCT
 451  TTCCAGCGCC GGGCAGGAGG GGTCCTGGTT GCTAGCCATC TGCAGAGCTT
 501  CCTGGAGGTG TCGTACCGCG TTCTACGCCA CCTTGCGCAG CCCTCTGGCG
 551  GCTCTGGCGG CTCTCAGAGC TTCCTGCTCA AGTCTTTAGA GCAAGTGAGA
 601  AAGATCCAGG GCGATGGCGC AGCGCTCCAG GAGAAGCTGT GTGCCACCTA
 651  CAAGCTGTGC CACCCCGAGG AGCTGGTGCT GCTCGGACAC TCTCTGGGCA
 701  TCCCCTGGGC TCCCCTGAGC TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA
 751  GGCTGCTTGA GCCAACTCCA TAGCGGCCTT TTCCTCTACC AGGGGCTCCT
 801  GCAGGCCCTG GAAGGGATAT CCCCCGAGTT GGGTCCCACC TTGGACACAC
 851  TGCAGCTGGA CGTCGCCGAC TTTGCCACCA CCATCTGGCA GCAGATGGAA
 901  GAACTGGGAA TGGCCCCTGC CCTGCAGCCC ACCCAGGGTG CCATGCCGGC
 951  CTTCGCCTAA TAA (SEQ ID NO:103)
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pMON13192

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   1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
  51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 101  CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
 151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 351  CGGTGGAGGC TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTT
 401  ACAAGCTGTG CCACCCCGAG GAGCTGGTGC TGCTCGGACA CTCTCTGGGC
 451  ATCCCCTGGG CTCCCCTGAG CTCCTGCCCC AGCCAGGCCC TGCAGCTGGC
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 501  AGGCTGCTTG AGCCAACTCC ATAGCGGCCT TTTCCTCTAC CAGGGGCTCC
 551  TGCAGGCCCT GGAAGGGATA TCCCCCGAGT TGGGTCCCAC CTTGGACACA
 601  CTGCAGCTGG ACGTCGCCGA CTTTGCCACC ACCATCTGGC AGCAGATGGA
 651  AGAACTGGGA ATGGCCCCTG CCCTGCAGCC CACCCAGGGT GCCATGCCGG
 701  CCTTCGCCTC TGCTTTCCAG CGCCGGGCAG GAGGGGTCCT GGTTGCTAGC
 751  CATCTGCAGA GCTTCCTGGA GGTGTCGTAC CGCGTTCTAC GCCACCTTGC
 801  GCAGCCCACA CCATTGGGCC CTGCCAGCTC CCTGCCCCAG AGCTTCCTGC
 851  TCAAGTCTTT AGAGCAAGTG AGAAAGATCC AGGGCGATGG CGCAGCGCTC
 901  CAGGAGAAGC TGTGTGCCAC CTAATAA (SEQ ID NO:104)
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pMON13193

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   1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
  51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 101  CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
 151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
 401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTTACAAG
 451  CTGTGCCACC CCGAGGAGCT GGTGCTGCTC GGACACTCTC TGGGCATCCC
 501  CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG CTGGCAGGCT
 551  GCTTGAGCCA ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG
 601  GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA
 651  GCTGGACGTC GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC
 701  TGGGAATGGC CCCTGCCCTG CAGCCCACCC AGGGTGCCAT GCCGGCCTTC
 751  GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG GTCCTGGTTG CTAGCCATCT
 801  GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC CTTGCGCAGC
 851  CCACACCATT GGGCCCTGCC AGCTCCCTGC CCCAGAGCTT CCTGCTCAAG
 901  TCTTTAGAGC AAGTGAGAAA GATCCAGGGC GATGGCGCAG CGCTCCAGGA
 951  GAAGCTGTGT GCCACCTAAT AA (SEQ ID NO:105)
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pMON25190

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   1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
  51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 101  CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
 151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 351  CGGTGGAGGC TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTC
 401  CCGAGTTGGG TCCCACCTTG GACACACTGC AGCTGGACGT CGCCGACTTT
 451  GCCACCACCA TCTGGCAGCA GATGGAAGAA CTGGGAATGG CCCCTGCCCT
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 501  GCAGCCCACC CAGGGTGCCA TGCCGGCCTT CGCCTCTGCT TTCCAGCGCC
 551  GGGCAGGAGG GGTCCTGGTT GCTAGCCATC TGCAGAGCTT CCTGGAGGTG
 601  TCGTACCGCG TTCTACGCCA CCTTGCGCAG CCCACACCAT TGGGCCCTGC
 651  CAGCTCCCTG CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG CAAGTGAGAA
 701  AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC
 751  AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT
 801  CCCCTGGGCT CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG
 851  GCTGCTTGAG CCAACTCCAT AGCGGCCTTT TCCTCTACCA GGGGCTCCTG
 901  CAGGCCCTGG AAGGGATATC CTAATAA (SEQ ID NO:106)
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pMON25191

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   1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
  51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 101  CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
 151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
 401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTCCCGAG
 451  TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC
 501  CACCATCTGG CAGCAGATGG AAGAACTGGG AATGGCCCCT GCCCTGCAGC
 551  CCACCCAGGG TGCCATGCCG GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA
 601  GGAGGGGTCC TGGTTGCTAG CCATCTGCAG AGCTTCCTGG AGGTGTCGTA
 651  CCGCGTTCTA CGCCACCTTG CGCAGCCCAC ACCATTGGGC CCTGCCAGCT
 701  CCCTGCCCCA GAGCTTCCTG CTCAAGTCTT TAGAGCAAGT GAGAAAGATC
 751  CAGGGCGATG GCGCAGCGCT CCAGGAGAAG CTGTGTGCCA CCTACAAGCT
 801  GTGCCACCCC GAGGAGCTGG TGCTGCTCGG ACACTCTCTG GGCATCCCCT
 851  GGGCTCCCCT GAGCTCCTGC CCCAGCCAGG CCCTGCAGCT GGCAGGCTGC
 901  TTGAGCCAAC TCCATAGCGG CCTTTTCCTC TACCAGGGGC TCCTGCAGGC
 951  CCTGGAAGGG ATATCCTAAT AA (SEQ ID NO:107)
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pMON13194

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   1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
  51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 101  CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
 151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 351  CGGTGGAGGC TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA
 401  TGGCCCCTGC CCTGCAGCCC ACCCAGGGTG CCATGCCGGC CTTCGCCTCT
 451  GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG GTTGCTAGCC ATCTGCAGAG
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 501  CTTCCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG CAGCCCACAC
 551  CATTGGGCCC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTCTTTA
 601  GAGCAAGTGA GAAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT
 651  GTGTGCCACC TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC
 701  ACTCTCTGGG CATCCCCTGG GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC
 751  CTGCAGCTGG CAGGCTGCTT GAGCCAACTC CATAGCGGCC TTTTCCTCTA
 801  CCAGGGGCTC CTGCAGGCCC TGGAAGGGAT ATCCCCCGAG TTGGGTCCCA
 851  CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG
 901  CAGCAGATGG AAGAACTGGG ATAATAA (SEQ ID NO:108)
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pMON13195

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   1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
  51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 101  CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
 151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
 401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTATGGCC
 451  CCTGCCCTGC AGCCCACCCA GGGTGCCATG CCGGCCTTCG CCTCTGCTTT
 501  CCAGCGCCGG GCAGGAGGGG TCCTGGTTGC TAGCCATCTG CAGAGCTTCC
 551  TGGAGGTGTC GTACCGCGTT CTACGCCACC TTGCGCAGCC CACACCATTG
 601  GGCCCTGCCA GCTCCCTGCC CCAGAGCTTC CTGCTCAAGT CTTTAGAGCA
 651  AGTGAGAAAG ATCCAGGGCG ATGGCGCAGC GCTCCAGGAG AAGCTGTGTG
 701  CCACCTACAA GCTGTGCCAC CCCGAGGAGC TGGTGCTGCT CGGACACTCT
 751  CTGGGCATCC CCTGGGCTCC CCTGAGCTCC TGCCCCAGCC AGGCCCTGCA
 801  GCTGGCAGGC TGCTTGAGCC AACTCCATAG CGGCCTTTTC CTCTACCAGG
 851  GGCTCCTGCA GGCCCTGGAA GGGATATCCC CCGAGTTGGG TCCCACCTTG
 901  GACACACTGC AGCTGGACGT CGCCGACTTT GCCACCACCA TCTGGCAGCA
 951  GATGGAAGAA CTGGGATAAT AA (SEQ ID NO:109)
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pMON13196

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   1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
  51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 101  CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
 151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 351  CGGTGGAGGC TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA
 401  CCCAGGGTGC CATGCCGGCC TTCGCCTCTG CTTTCCAGCG CCGGGCAGGA
 451  GGGGTCCTGG TTGCTAGCCA TCTGCAGAGC TTCCTGGAGG TGTCGTACCG
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  501  CGTTCTACGC CACCTTGCGC AGCCCACACC ATTGGGCCCT GCCAGCTCCC
  551  TGCCCCAGAG CTTCCTGCTC AAGTCTTTAG AGCAAGTGAG AAAGATCCAG
  601  GGCGATGGCG CAGCGCTCCA GGAGAAGCTG TGTGCCACCT ACAAGCTGTG
  651  CCACCCCGAG GAGCTGGTGC TGCTCGGACA CTCTCTGGGC ATCCCCTGGG
  701  CTCCCCTGAG CTCCTGCCCC AGCCAGGCCC TGCAGCTGGC AGGCTGCTTG
  751  AGCCAACTCC ATAGCGGCCT TTTCCTCTAC CAGGGGCTCC TGCAGGCCCT
  801  GGAAGGGATA TCCCCCGAGT TGGGTCCCAC CTTGGACACA CTGCAGCTGG
  851  ACGTCGCCGA CTTTGCCACC ACCATCTGGC AGCAGATGGA AGAACTGGGA
  901  ATGGCCCCTG CCCTGCAGCC CTAATAA (SEQ ID NO:110)
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pMON13197

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    1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
   51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
  101  CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
  151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
  201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
  251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
  301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
  351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
  401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTACCCAG
  451  GGTGCCATGC CGGCCTTCGC CTCTGCTTTC CAGCGCCGGG CAGGAGGGGT
  501  CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG TACCGCGTTC
  551  TACGCCACCT TGCGCAGCCC ACACCATTGG GCCCTGCCAG CTCCCTGCCC
  601  CAGAGCTTCC TGCTCAAGTC TTTAGAGCAA GTGAGAAAGA TCCAGGGCGA
  651  TGGCGCAGCG CTCCAGGAGA AGCTGTGTGC CACCTACAAG CTGTGCCACC
  701  CCGAGGAGCT GGTGCTGCTC GGACACTCTC TGGGCATCCC CTGGGCTCCC
  751  CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG CTGGCAGGCT GCTTGAGCCA
  801  ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG GCCCTGGAAG
  851  GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC
  901  GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC
  951  CCCTGCCCTG CAGCCCTAAT AA (SEQ ID NO:111)
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pMON13198

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    1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
   51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
  101  CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
  151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
  201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
  251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
  301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
  351  CGGTGGAGGC TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTT
  401  CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG
  451  AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCAC
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 501  ACCATTGGGC CCTGCCAGCT CCCTGCCCCA GAGCTTCCTG CTCAAGTCTT
 551  TAGAGCAAGT GAGAAAGATC CAGGGCGATG GCGCAGCGCT CCAGGAGAAG
 601  CTGTGTGCCA CCTACAAGCT GTGCCACCCC GAGGAGCTGG TGCTGCTCGG
 651  ACACTCTCTG GGCATCCCCT GGGCTCCCCT GAGCTCCTGC CCCAGCCAGG
 701  CCCTGCAGCT GGCAGGCTGC TTGAGCCAAC TCCATAGCGG CCTTTTCCTC
 751  TACCAGGGGC TCCTGCAGGC CCTGGAAGGG ATATCCCCCG AGTTGGGTCC
 801  CACCTTGGAC ACACTGCAGC TGGACGTCGC CGACTTTGCC ACCACCATCT
 851  GGCAGCAGAT GGAAGAACTG GGAATGGCCC CTGCCCTGCA GCCCACCCAG
 901  GGTGCCATGC CGGCCTTCGC CTAATAA (SEQ ID NO:112)
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pMON13199

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   1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
  51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 101  CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
 151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
 401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTTCTGCT
 451  TTCCAGCGCC GGGCAGGAGG GGTCCTGGTT GCTAGCCATC TGCAGAGCTT
 501  CCTGGAGGTG TCGTACCGCG TTCTACGCCA CCTTGCGCAG CCCACACCAT
 551  TGGGCCCTGC CAGCTCCCTG CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG
 601  CAAGTGAGAA AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG
 651  TGCCACCTAC AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG CTCGGACACT
 701  CTCTGGGCAT CCCCTGGGCT CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG
 751  CAGCTGGCAG GCTGCTTGAG CCAACTCCAT AGCGGCCTTT TCCTCTACCA
 801  GGGGCTCCTG CAGGCCCTGG AAGGGATATC CCCCGAGTTG GGTCCCACCT
 851  TGGACACACT GCAGCTGGAC GTCGCCGACT TTGCCACCAC CATCTGGCAG
 901  CAGATGGAAG AACTGGGAAT GGCCCCTGCC CTGCAGCCCA CCCAGGGTGC
 951  CATGCCGGCC TTCGCCTAAT AA (SEQ ID NO:113)
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pMON31112

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   1  ATGGCTAACT GCTCTAACAT GATCGATGAA ATCATCACCC ACCTGAAGCA
  51  GCCACCGCTG CCGCTGCTGG ACTTCAACAA CCTCAATGGT GAAGACCAAG
 101  ATATCCTAAT GGACAATAAC CTTCGTCGTC CAAACCTCGA GGCATTCAAC
 151  CGTGCTGTCA AGTCTCTGCA GAATGCATCA GCAATTGAGA GCATTCTTAA
 201  AAATCTCCTG CCATGTCTGC CGCTAGCCAC GGCCGCACCC ACGCGACATC
 251  CAATCCATAT CAAGGACGGT GACTGGAATG AATTCCGTCG TAAACTGACC
 301  TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAGT ACGTAGAGGG
 351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
 401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTACCCAG
 451  GGTGCCATGC CGGCCTTCGC CTCTGCTTTC CAGCGCCGGG CAGGAGGGGT
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  501  CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG TACCGCGTTC
  551  TACGCCACCT TGCGCAGCCC TCTGGCGGCT CTGGCGGCTC TCAGAGCTTC
  601  CTGCTCAAGT CTTTAGAGCA AGTGAGAAAG ATCCAGGGCG ATGGCGCAGC
  651  GCTCCAGGAG AAGCTGTGTG CCACCTACAA GCTGTGCCAC CCCGAGGAGC
  701  TGGTGCTGCT CGGACACTCT CTGGGCATCC CCTGGGCTCC CCTGAGCTCC
  751  TGCCCCAGCC AGGCCCTGCA GCTGGCAGGC TGCTTGAGCC AACTCCATAG
  801  CGGCCTTTTC CTCTACCAGG GGCTCCTGCA GGCCCTGGAA GGGATATCCC
  851  CCGAGTTGGG TCCCACCTTG GACACACTGC AGCTGGACGT CGCCGACTTT
  901  GCCACCACCA TCTGGCAGCA GATGGAAGAA CTGGGAATGG CCCCTGCCCT
  951  GCAGCCCTAA TAA (SEQ ID NO:114)
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pMON31113

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    1  ATGGCTAACT GCTCTAACAT GATCGATGAA ATCATCACCC ACCTGAAGCA
   51  GCCACCGCTG CCGCTGCTGG ACTTCAACAA CCTCAATGGT GAAGACCAAG
  101  ATATCCTGAT GGAAAATAAC CTTCGTCGTC CAAACCTCGA GGCATTCAAC
  151  CGTGCTGTCA AGTCTCTGCA GAATGCATCA GCAATTGAGA GCATTCTTAA
  201  AAATCTCCTG CCATGTCTGC CCCTGGCCAC GGCCGCACCC ACGCGACATC
  251  CAATCATCAT CCGTGACGGT GACTGGAATG AATTCCGTCG TAAACTGACC
  301  TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAGT ACGTAGAGGG
  351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
  401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTACCCAG
  451  GGTGCCATGC CGGCCTTCGC CTCTGCTTTC CAGCGCCGGG CAGGAGGGGT
  501  CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG TACCGCGTTC
  551  TACGCCACCT TGCGCAGCCC ACACCATTGG GCCCTGCCAG CTCCCTGCCC
  601  CAGAGCTTCC TGCTCAAGTC TTTAGAGCAA GTGAGAAAGA TCCAGGGCGA
  651  TGGCGCAGCG CTCCAGGAGA AGCTGTGTGC CACCTACAAG CTGTGCCACC
  701  CCGAGGAGCT GGTGCTGCTC GGACACTCTC TGGGCATCCC CTGGGCTCCC
  751  CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG CTGGCAGGCT GCTTGAGCCA
  801  ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG GCCCTGGAAG
  851  GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC
  901  GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC
  951  CCCTGCCCTG CAGCCCTAAT AA (SEQ ID NO:115)
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pMON31114

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    1  ATGGCTAACT GCTCTAACAT GATCGATGAA ATCATCACCC ACCTGAAGCA
   51  GCCACCGCTG CCGCTGCTGG ACTTCAACAA CCTCAATGGT GAAGACCAAG
  101  ATATCCTGAT GGAAAATAAC CTTCGTCGTC CAAACCTCGA GGCATTCAAC
  151  CGTGCTGTCA AGTCTCTGCA GAATGCATCA GCAATTGAGA GCATTCTTAA
  201  AAATCTCCTG CCATGTCTGC CCCTGGCCAC GGCCGCACCC ACGCGACATC
  251  CAATCATCAT CCGTGACGGT GACTGGAATG AATTCCGTCG TAAACTGACC
  301  TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAGT ACGTAGAGGG
  351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
  401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTACCCAG
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  451  GGTGCCATGC CGGCCTTCGC CTCTGCTTTC CAGCGCCGGG CAGGAGGGGT
  501  CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG TACCGCGTTC
  551  TACGCCACCT TGCGCAGCCC TCTGGCGGCT CTGGCGGCTC TCAGAGCTTC
  601  CTGCTCAAGT CTTTAGAGCA AGTGAGAAAG ATCCAGGGCG ATGGCGCAGC
  651  GCTCCAGGAG AAGCTGTGTG CCACCTACAA GCTGTGCCAC CCCGAGGAGC
  701  TGGTGCTGCT CGGACACTCT CTGGGCATCC CCTGGGCTCC CCTGAGCTCC
  751  TGCCCCAGCC AGGCCCTGCA GCTGGCAGGC TGCTTGAGCC AACTCCATAG
  801  CGGCCTTTTC CTCTACCAGG GGCTCCTGCA GGCCCTGGAA GGGATATCCC
  851  CCGAGTTGGG TCCCACCTTG GACACACTGC AGCTGGACGT CGCCGACTTT
  901  GCCACCACCA TCTGGCAGCA GATGGAAGAA CTGGGAATGG CCCCTGCCCT
  951  GCAGCCCTAA TAA (SEQ ID NO:116)
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pMON31115

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    1  ATGGCTAACT GCTCTAACAT GATCGATGAA ATCATCACCC ACCTGAAGCA
   51  GCCACCGCTG CCGCTGCTGG ACTTCAACAA CCTCAATGGT GAAGACCAAG
  101  ATATCCTAAT GGACAATAAC CTTCGTCGTC CAAACCTCGA GGCATTCAAC
  151  CGTGCTGTCA AGTCTCTGCA GAATGCATCA GCAATTGAGA GCATTCTTAA
  201  AAATCTCCTG CCATGTCTGC CGCTAGCCAC GGCCGCACCC ACGCGACATC
  251  CAATCCATAT CAAGGACGGT GACTGGAATG AATTCCGTCG TAAACTGACC
  301  TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAGT ACGTAGAGGG
  351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
  401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTACCCAG
  451  GGTGCCATGC CGGCCTTCGC CTCTGCTTTC CAGCGCCGGG CAGGAGGGGT
  501  CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG TACCGCGTTC
  551  TACGCCACCT TGCGCAGCCC ACACCATTGG GCCCTGCCAG CTCCCTGCCC
  601  CAGAGCTTCC TGCTCAAGTC TTTAGAGCAA GTGAGAAAGA TCCAGGGCGA
  651  TGGCGCAGCG CTCCAGGAGA AGCTGTGTGC CACCTACAAG CTGTGCCACC
  701  CCGAGGAGCT GGTGCTGCTC GGACACTCTC TGGGCATCCC CTGGGCTCCC
  751  CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG CTGGCAGGCT GCTTGAGCCA
  801  ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG GCCCTGGAAG
  851  GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC
  901  GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC
  951  CCCTGCCCTG CAGCCCTAAT AA (SEQ ID NO:117)
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pMON28505

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GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
CATGGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGCCTGCTGTGGACTTTAGCTTGGGAG
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AATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTGACCCTTCTG
CTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCCCTCCTGGG
GCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGC
TTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAA
CACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAG
GGAATTCGGCGGCAACATGGCGTCTCCCGCTCCGCCTGCTTGTGACCTCCGAGTCCTCAGTA
AACTGCTTCGTGACTCCCATGTCCTTCACAGCAGACTGAGCCAGTGCCCA (SEQ ID NO:118)

pMON28506

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
CATGTTGCCTACACCTGTCCTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCC
AGATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTG
ATGGCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGG
ACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGG
GCAGGACCACAGCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGA
GGAAAGGTGCGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGAATTCGGCGG
CAACATGGCGTCTCCCGCTCCGCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTG
ACTCCCATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCT (SEQ ID NO:119)

pMON28507

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
CATGGTCCTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGA
CCAAGGCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGG
GGACAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCT
CCTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAG
CTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGT
TTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGAATTCGGCGGCAACATGGCGTC
TCCCGCTCCGCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCC

TTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCT (SEQ ID NO:120)

pMON28508

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
CATGGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGG
ACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGA
CCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGC
CCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATC
CCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTT
GTAGGAGGGTCCACCCTCTGCGTCAGGGAATTCGGCGGCAACATGGCGTCTCCCGCTCCGCC
TGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCACAGCAGAC
TGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGCCT (SEQ ID NO:121)

pMON28509

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
CATGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTC
TGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACCCACT
TGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCA
GAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCCAATG
CCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGTAGGA
GGGTCCACCCTCTGCGTCAGGGAATTCGGCGGCAACATGGCGTCTCCCGCTCCGCCTGCTTG
TGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCACAGCAGACTGAGCC
AGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGCCTGCTGTG (SEQ ID NO:122)

pMON28510

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCGGTTAC
CCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGGAACCGTC
TGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAACTCCAAACAT
GGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTGGAGCAGTGACCCT
TCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACCCACTTGCTCTCATCCCTCCT
GGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGGCCTCCTTGGAACCCA
GCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCCAATGCATCTTCCTGAGCTTCCA
ACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGTAGGGGGTCCACCCTCTGCGTCAG
GGAATTCGGCGGCAACATGGCGTCTCCCGCTCCGCCTGCTGTGACCTCCGAGTCCTCAGTAA
ACTGCTTCGTGACTCCCATGTCCTTCACAGCAGACTGACCAGTGCCCAGAGGTTCACCCTTT
GCCTACACCTGTCCTGCTGCCTGCTGTGGACTTTAGTTG (SEQ ID NO:123)

pMON28511

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
CATGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCC
TTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCAC
AAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCT
GATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGAATTCGGCGGCAACATGGCGTCTCCCG
CTCCGCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCAC
AGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGCCTGCTGT
GGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTGG
GAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTG (SEQ ID
NO:124)

pMON28512

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
CATGGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCCAATGCCATCT

TCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGTAGGAGGGTCC
ACCCTCTGCGTCAGGGAATTCGGCGGCAACATGGCGTCTCCCGCTCCGCCTGCTTGTGACCT
CCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCACAGCAGACTGAGCCAGTGCC
CAGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAA
TGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTGACCCTTCTGCT
GGAGGGAGTGATGGCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGGC
AGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGAGCCTCCTT (SEQ ID NO:125)

pMON28513

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
CATGGGCAGGACCACAGCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGC
TCCGAGGAAAGGTGCGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGAATTC
GGCGGCAACATGGCGTCTCCCGCTCCGCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCT
TCGTGACTCCCATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTA
CACCTGTCCTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAG
ACCAAGGCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACG
GGGACAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTC
TCCTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAG (SEQ ID NO:126)

pMON28514

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
CATGGCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGG
TGCGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGAATTCGGCGGCAACATG
GCGTCTCCCGCTCCGCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCA
TGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGC
TGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAG
GACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGG
ACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGG

CCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACA (SEQ ID NO:127)

pMON28515

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
CATGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCC
TGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGAATTCGGCGGCAACATGGCGTCTCCC
GCTCCGCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCA
CAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGCCTGCTG
TGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTG
GGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACCCACTTG
CCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGA
GCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAG (SEQ ID NO:128)

pMON28516

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
CATGGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTG
TAGGAGGGTCCACCCTCTGCGTCAGGGAATTCGGCGGCAACATGGCGTCTCCCGCTCCGCCT
GCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCACAGCAGACT
GAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGCCTGCTGTGGACTTTA
GCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTG
ACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATC
CCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGAGCCTCCTTG
GAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCCAAT (SEQ ID NO:129)

pMON28519

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
CATGGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGCCTGCTGTGGACTTTAGCTTGGGAG
AATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTGACCCTTCTG
CTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCCCTCCTGGG
GCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGC
TTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAA
CACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAG
GGAATTCGGCAACATGGCGTCTCCCGCTCCGCCTGCTTGTGACCTCCGAGTCCTCAGTAAAC
TGCTTCGTGACTCCCATGTCCTTCACAGCAGACTGAGCCAGTGCCCA (SEQ ID NO:130)

pMON28520

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
CATGTTGCCTACACCTGTCCTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCC
AGATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTG
ATGGCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGG
ACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGG
GCAGGACCACAGCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGA
GGAAAGGTGCGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGAATTCGGCAA
CATGGCGTCTCCCGCTCCGCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACT
CCCATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCT (SEQ ID NO:131)

pMON28521

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA

CATGGTCCTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGA
CCAAGGCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGG
GGACAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCT
CCTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAG
CTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGT
TTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGAATTCGGCAACATGGCGTCTCC
CGCTCCGCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTC
ACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCT (SEQ ID NO:132)

pMON28522

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
CATGGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGG
ACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGA
CCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGC
CCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATC
CCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTT
GTAGGAGGGTCCACCCTCTGCGTCAGGGAATTCGGCAACATGGCGTCTCCCGCTCCGCCTGC
TTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCACAGCAGACTGA
GCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGCCT (SEQ ID NO:133)

pMON28523

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
CATGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTC
TGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACCCACT
TGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCA
GAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCCAATG
CCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGTAGGA
GGGTCCACCCTCTGCGTCAGGGAATTCGGCAACATGGCGTCTCCCGCTCCGCCTGCTTGTGA
CCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCACAGCAGACTGAGCCAGT

GCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGCCTGCTGTG (SEQ ID NO:134)

pMON28524

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
CATGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTGA
CCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCC
CTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGAGCCTCCTTGG
AACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCCAATGCCATCTTCCTGA
GCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGTAGGAGGGTCCACCCTC
TGCGTCAGGGAATTCGGCAACATGGCGTCTCCCGCTCCGCCTGCTTGTGACCTCCGAGTCCT
CAGTAAACTGCTTCGTGACTCCCATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTC
ACCCTTTGCCTACACCTGTCCTGCTGCCTGCTGTGGACTTTAGCTTG (SEQ ID NO:135)

pMON28525

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
CATGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCC
TTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCAC
AAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCT
GATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGAATTCGGCAACATGGCGTCTCCCGCTC
CGCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCACAGC
AGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGCCTGCTGTGGA
CTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTGGGAG
CAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTG (SEQ ID NO:136)

pMON28526

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
CATGGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCCAATGCCATCT
TCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGTAGGAGGGTCC
ACCCTCTGCGTCAGGGAATTCGGCAACATGGCGTCTCCCGCTCCGCCTGCTTGTGACCTCCG
AGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCACAGCAGACTGAGCCAGTGCCCAG
AGGTTCACCCTTTGCCTACACCTGTCCTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGG
AAAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGA
GGGAGTGATGGCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGC
TTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGAGCCTCCTT (SEQ ID NO:137)

pMON28527

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
CATGGGCAGGACCACAGCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGC
TCCGAGGAAAGGTGCGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGAATTC
GGCAACATGGCGTCTCCCGCTCCGCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCG
TGACTCCCATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACAC
CTGTCCTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACC
AAGGCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGG
ACAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCC
TCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAG (SEQ ID NO:138)

pMON28528

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA

CATGGCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGG
TGCGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGAATTCGGCAACATGGCG
TCTCCCGCTCCGCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGT
CCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGC
CTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGAC
ATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACC
CACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCC
TGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACA (SEQ ID NO:139)

pMON28529

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
CATGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCC
TGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGAATTCGGCAACATGGCGTCTCCCGCT
CCGCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCACAG
CAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGCCTGCTGTGG
ACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTGGGA
GCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACCCACTTGCCT
CTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGAGCC
TCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAG (SEQ ID NO:140)

pMON28530

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
CATGGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTG
TAGGAGGGTCCACCCTCTGCGTCAGGGAATTCGGCAACATGGCGTCTCCCGCTCCGCCTGCT
TGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCACAGCAGACTGAG
CCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGCCTGCTGTGGACTTTAGCT
TGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTGACC
CTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCCCT
CCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGAGCCTCCTTGGAA

CCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCCAAT (SEQ ID NO:141)

pMON28533

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTGACT
TCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATGAGGC
AATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGCATCCAAT
CATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATTGGTTACCCT
TGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGTAACCGTCTGGT
CCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAACATGGA
GGTTCACCCTTTGCCTACACCTGTCCTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGA
AAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGAG
GGAGTGATGGCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCT
TTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTC
CACAGGGCAGGACCACAGCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTG
CTCCGAGGAAAGGTGCGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGAATT
CGGCGGCAACGGCGGCAACATGGCGTCCCCAGCGCCGCCTGCTTGTGACCTCCGAGTCCTCA
GTAAACTGCTTCGTGACTCCCATGTCCTTCACAGCAGACTGAGCCAGTGCCCA (SEQ ID NO:142)

pMON28534

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
CATGTTGCCTACACCTGTCCTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCC
AGATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTG
ATGGCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGG
ACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGG
GCAGGACCACAGCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGA
GGAAAGGTGCGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGAATTCGGCGG
CAACGGCGGCAACATGGCGTCCCCAGCGCCGCCTGCTTGTGACCTCCGAGTCCTCAGTAAAC
TGCTTCGTGACTCCCATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCT
(SEQ ID NO:143)

pMON28535

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
CATGGTCCTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGA
CCAAGGCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGG
GGACAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCT
CCTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAG
CTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGT
TTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGAATTCGGCGGCAACGGCGGCAA
CATGGCGTCCCCAGCGCCGCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACT
CCCATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCT
(SEQ ID NO:144)

pMON28536

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
CATGGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGG
ACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGA
CCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGC
CCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATC
CCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTT
GTAGGAGGGTCCACCCTCTGCGTCAGGGAATTCGGCGGCAACGGCGGCAACATGGCGTCCCC
AGCGCCGCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTC
ACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGCCT
(SEQ ID NO:145)

pMON28537

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA

CATGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTC
TGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACCCACT
TGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCA
GAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCCAATG
CCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGTAGGA
GGGTCCACCCTCTGCGTCAGGGAATTCGGCGGCAACGGCGGCAACATGGCGTCCCCAGCGCC
GCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCACAGCA
GACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGCCTGCTGTG
(SEQ ID NO:146)

pMON28538

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
CATGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTGA
CCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCC
CTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGAGCCTCCTTGG
AACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCCAATGCCATCTTCCTGA
GCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGTAGGAGGGTCCACCCTC
TGCGTCAGGGAATTCGGCGGCAACGGCGGCAACATGGCGTCCCCAGCGCCGCCTGCTTGTGA
CCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCACAGCAGACTGAGCCAGT
GCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGCCTGCTGTGGACTTTAGCTTG
(SEQ ID NO:147)

pMON28539

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
CATGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCC
TTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCAC
AAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCT
GATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGAATTCGGCGGCAACGGCGGCAACATGG
CGTCCCCAGCGCCGCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCAT
GTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCT

GCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGG
ACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTG
(SEQ ID NO:148)

pMON28540

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
CATGGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCCAATGCCATCT
TCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGTAGGAGGGTCC
ACCCTCTGCGTCAGGGAATTCGGCGGCAACGGCGGCAACATGGCGTCCCCAGCGCCGCCTGC
TTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCACAGCAGACTGA
GCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGCCTGCTGTGGACTTTAGC
TTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTGAC
CCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCCC
TCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGAGCCTCCTT
(SEQ ID NO:149)

pMON28541

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
CATGGGCAGGACCACAGCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGC
TCCGAGGAAAGGTGCGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGAATTC
GGCGGCAACGGCGGCAACATGGCGTCCCCAGCGCCGCCTGCTTGTGACCTCCGAGTCCTCAG
TAAACTGCTTCGTGACTCCCATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACC
CTTTGCCTACACCTGTCCTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAG
ATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGAT
GGCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGAC
AGGTCCGTCTCCTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAG
(SEQ ID NO:150)

pMON28542

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
CATGGCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGG
TGCGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGAATTCGGCGGCAACGGC
GGCAACATGGCGTCCCCAGCGCCGCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCG
TGACTCCCATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACAC
CTGTCCTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACC
AAGGCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGG
ACAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCC
TCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACA
(SEQ ID NO:151)

pMON28543

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
CATGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCC
TGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGAATTCGGCGGCAACGGCGGCAACATG
GCGTCCCCAGCGCCGCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCA
TGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGC
TGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAG
GACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGG
ACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGG
CCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAG
(SEQ ID NO:152)

pMON28544

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA

CATGGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTG
TAGGAGGGTCCACCCTCTGCGTCAGGGAATTCGGCGGCAACGGCGGCAACATGGCGTCCCCA
GCGCCGCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCA
CAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGCCTGCTG
TGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTG
GGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACCCACTTG
CCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGA
GCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCCAAT
(SEQ ID NO:153)

pMON28545

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
CATGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCC
TGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGAATTCGGCGGCAACATGGCGTCTCCC
GCTCCGCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCA
CAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGCCTGCTG
TGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTG
GGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACCCACTTG
CCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGA
GCCTCCTTGGAACCCAGGGCAGGACCACAGCTCACAAG (SEQ ID NO:154)

pMON15981

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  1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
 51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
101  CTATCCTGAT GGATCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GTCTTACAAG
451  CTGTGCCACC CCGAGGAGCT GGTGCTGCTC GGACACTCTC TGGGCATCCC
501  CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG CTGGCAGGCT
551  GCTTGAGCCA ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG
601  GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA
651  GCTGGACGTC GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC
701  TGGGAATGGC CCCTGCCCTG CAGCCCACCC AGGGTGCCAT GCCGGCCTTC
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751  GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG GTCCTGGTTG CTAGCCATCT
801  GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC CTTGCGCAGC
851  CCGGCGGCGG CTCTGACATG GCTACACCAT TAGGCCCTGC CAGCTCCCTG
901  CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG CAAGTGAGGA AGATCCAGGG
951  CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAA TAA;
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(SEQ ID NO:155)

pMON15982

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  1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
 51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
101  CTATCCTGAT GGATCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GTCTCCCGAG
451  TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC
501  CACCATCTGG CAGCAGATGG AAGAACTGGG AATGGCCCCT GCCCTGCAGC
551  CCACCCAGGG TGCCATGCCG GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA
601  GGAGGGGTCC TGGTTGCTAG CCATCTGCAG AGCTTCCTGG AGGTGTCGTA
651  CCGCGTTCTA CGCCACCTTG CGCAGCCCGG CGGCGGCTCT GACATGGCTA
701  CACCATTAGG CCCTGCCAGC TCCCTGCCCC AGAGCTTCCT GCTCAAGTCT
751  TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT GGCGCAGCGC TCCAGGAGAA
801  GCTGTGTGCC ACCTACAAGC TGTGCCACCC CGAGGAGCTG GTGCTGCTCG
851  GACACTCTCT GGGCATCCCC TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG
901  GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA CTCCATAGCG GCCTTTTCCT
951  CTACCAGGGG CTCCTGCAGG CCCTGGAAGG GATATCCTAA TAA;
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(SEQ ID NO:156)

pMON15965

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  1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
 51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
101  CTATCCTGAT GGATCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GTCTTCTGCT
451  TTCCAGCGCC GGGCAGGAGG GGTCCTGGTT GCTAGCCATC TGCAGAGCTT
501  CCTGGAGGTG TCGTACCGCG TTCTACGCCA CCTTGCGCAG CCCGGCGGCG
551  GCTCTGACAT GGCTACACCA TTAGGCCCTG CCAGCTCCCT GCCCCAGAGC
601  TTCCTGCTCA AGTCTTTAGA GCAAGTGAGG AAGATCCAGG GCGATGGCGC
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651  AGCGCTCCAG GAGAAGCTGT GTGCCACCTA CAAGCTGTGC CACCCCGAGG
701  AGCTGGTGCT GCTCGGACAC TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC
751  TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA GGCTGCTTGA GCCAACTCCA
801  TAGCGGCCTT TTCCTCTACC AGGGGCTCCT GCAGGCCCTG GAAGGGATAT
851  CCCCCGAGTT GGGTCCCACC TTGGACACAC TGCAGCTGGA CGTCGCCGAC
901  TTTGCCACCA CCATCTGGCA GCAGATGGAA GAACTGGGAA TGGCCCCTGC
951  CCTGCAGCCC ACCCAGGGTG CCATGCCGGC CTTCGCCTAA TAA
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(SEQ ID NO:157)

pMON15966

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  1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
 51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
101  CTATCCTGAT GGATCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GTCTATGGCC
451  CCTGCCCTGC AGCCCACCCA GGGTGCCATG CCGGCCTTCG CCTCTGCTTT
501  CCAGCGCCGG GCAGGAGGGG TCCTGGTTGC TAGCCATCTG CAGAGCTTCC
551  TGGAGGTGTC GTACCGCGTT CTACGCCACC TTGCGCAGCC CGGCGGCGGC
601  TCTGACATGG CTACACCATT AGGCCCTGCC AGCTCCCTGC CCCAGAGCTT
651  CCTGCTCAAG TCTTTAGAGC AAGTGAGGAA GATCCAGGGC GATGGCGCAG
701  CGCTCCAGGA GAAGCTGTGT GCCACCTACA AGCTGTGCCA CCCCGAGGAG
751  CTGGTGCTGC TCGGACACTC TCTGGGCATC CCCTGGGCTC CCCTGAGCTC
801  CTGCCCCAGC CAGGCCCTGC AGCTGGCAGG CTGCTTGAGC CAACTCCATA
851  GCGGCCTTTT CCTCTACCAG GGGCTCCTGC AGGCCCTGGA AGGGATATCC
901  CCCGAGTTGG GTCCCACCTT GGACACACTG CAGCTGGACG TCGCCGACTT
951  TGCCACCACC ATCTGGCAGC AGATGGAAGA ACTGGGATAA TAA
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(SEQ ID NO:158)

pMON15967

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  1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
 51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
101  CTATCCTGAT GGATCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GTCTACCCAG
451  GGTGCCATGC CGGCCTTCGC CTCTGCTTTC CAGCGCCGGG CAGGAGGGGT
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 501  CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG TACCGCGTTC
 551  TACGCCACCT TGCGCAGCCC GGCGGCGGCT CTGACATGGC TACACCATTA
 601  GGCCCTGCCA GCTCCCTGCC CCAGAGCTTC CTGCTCAAGT CTTTAGAGCA
 651  AGTGAGGAAG ATCCAGGGCG ATGGCGCAGC GCTCCAGGAG AAGCTGTGTG
 701  CCACCTACAA GCTGTGCCAC CCCGAGGAGC TGGTGCTGCT CGGACACTCT
 751  CTGGGCATCC CCTGGGCTCC CCTGAGCTCC TGCCCCAGCC AGGCCCTGCA
 801  GCTGGCAGGC TGCTTGAGCC AACTCCATAG CGGCCTTTTC CTCTACCAGG
 851  GGCTCCTGCA GGCCCTGGAA GGGATATCCC CCGAGTTGGG TCCCACCTTG
 901  GACACACTGC AGCTGGACGT CGCCGACTTT GCCACCACCA TCTGGCAGCA
 951  GATGGAAGAA CTGGGAATGG CCCCTGCCCT GCAGCCCTAA TAA
       (SEQ ID NO:159)
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pMON15960

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   1  ATGGCTACAC CATTGGGCCC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT
  51  CAAGTCTTTA GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC
 101  AGGAGAAGCT GTGTGCCACC TACAAGCTGT GCCACCCCGA GGAGCTGGTG
 151  CTGCTCGGAC ACTCTCTGGG CATCCCCTGG GCTCCCCTGA GCTCCTGCCC
 201  CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC CATAGCGGCC
 251  TTTTCCTCTA CCAGGGGCTC CTGCAGGCCC TGGAAGGGAT ATCCCCCGAG
 301  TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC
 351  CACCATCTGG CAGCAGATGG AAGAACTGGG AATGGCCCCT GCCCTGCAGC
 401  CCACCCAGGG TGCCATGCCG GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA
 451  GGAGGGGTCC TGGTTGCTAG CCATCTGCAG AGCTTCCTGG AGGTGTCGTA
 501  CCGCGTTCTA CGCCACCTTG CGCAGCCCGG CGGCGGCTCT GACATGGCTA
 551  CACCATTGGG CCCTGCCAGC TCCCTGCCCC AGAGCTTCCT GCTCAAGTCT
 601  TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT GGCGCAGCGC TCCAGGAGAA
 651  GCTGTGTGCC ACCTACAAGC TGTGCCACCC CGAGGAGCTG GTGCTGCTCG
 701  GACACTCTCT GGGCATCCCC TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG
 751  GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA CTCCATAGCG GCCTTTTCCT
 801  CTACCAGGGG CTCCTGCAGG CCCTGGAAGG GATATCCCCC GAGTTGGGTC
 851  CCACCTTGGA CACACTGCAG CTGGACGTCG CCGACTTTGC CACCACCATC
 901  TGGCAGCAGA TGGAAGAACT GGGAATGGCC CCTGCCCTGC AGCCCACCCA
1001  TCCTGGTTGC TAGCCATCTG CAGAGCTTCC TGGAGGTGTC GTACCGCGTT
1051  CTACGCCACC TTGCGCAGCC CTGATAA (SEQ ID NO:160)
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PMON32132

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TCTCCCGCTCCGCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGT
CCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGC
CTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGAC
ATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACC
CACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCC
TGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCC
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AATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGT
AGGAGGGTCCACCCTCTGCGTCAGG
(SEQ ID NO:249)

PMON32133

TCTCCCGCTCCGCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGT
CCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGC
CTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGAC
ATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACC
CACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCC
TGCAGAGCCTCCTTGGAACCCAGGGCAGGACCACAGCTCACAAGGATCCCAATGCCATCTTC
CTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGTAGGAGGGTCCAC
CCTCTGCGTCAGG (SEQ ID NO:250)

pMON32134

TCCCCAGCGCCGCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGT
CCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGC
CTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGAC
ATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACC
CACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCC
TGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCC
AATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGT
AGGAGGGTCCACCCTCTGCGTCAGG
(SEQ ID NO:251)

Pmon13181

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  1  CCATGGCTAA CTGCTCTATA ATGATCGATG AAATTATACA TCACTTAAAG
 51  AGACCACCTG CACCTTTGCT GGACCCGAAC AACCTCAATG ACGAAGACGT
101  CTCTATCCTG ATGGATCGAA ACCTTCGACT TCCAAACCTG GAGAGCTTCG
151  TAAGGGCTGT CAAGAACTTA GAAAATGCAT CAGGTATTGA GGCAATTCTT
201  CGTAATCTCC AACCATGTCT GCCCTCTGCC ACGGCCGCAC CCTCTCGACA
251  TCCAATCATC ATCAAGGCAG GTGACTGGCA AGAATTCCGG GAAAAACTGA
301  CGTTCTATCT GGTTACCCTT GAGCAAGCGC AGGAACAACA GTACGTAgag
351  ggcggtggag gctcCCCGGG TGAACCGTCT GGTCCAATCT CTACTATCAA
401  CCCGTCTCCT CCGTCTAAAG AATCTCATAA ATCTCCAAAC ATGTAAGGTA
451  CCGCATGCAA GCTT (SEQ ID NO:257)
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Pmon13180.Seg

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  1  CCATGGCTAA CTGCTCTATA ATGATCGATG AAATTATACA TCACTTAAAG
 51  AGACCACCTG CACCTTTGCT GGACCCGAAC AACCTCAATG ACGAAGACGT
101  CTCTATCCTG ATGGATCGAA ACCTTCGACT TCCAAACCTG GAGAGCTTCG
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151  TAAGGGCTGT CAAGAACTTA GAAAATGCAT CAGGTATTGA GGCAATTCTT
201  CGTAATCTCC AACCATGTCT GCCCTCTGCC ACGGCCGCAC CCTCTCGACA
251  TCCAATCATC ATCAAGGCAG GTGACTGGCA AGAATTCCGG GAAAAACTGA
301  CGTTCTATCT GGTTACCCTT GAGCAAGCGC AGGAACAACA GTACGTAgag
351  ggcggtggag gctcCCCGGG TGGTGGTTCT GGCGGCGGCT CCAACATGTA
401  AGGTACCGCA TGCAAGCTT (SEQ ID NO:258)
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pmon16017.seq

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  1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
 51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
101  CTATCCTGAT GGATCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTTTAGGC
451  CCTGCCAGCT CCCTGCCCCA GAGCTTCCTG CTCAAGTCTT TAGAGCAAGT
501  GAGGAAGATC CAGGGCGATG GCGCAGCGCT CCAGGAGAAG CTGTGTGCCA
551  CCTACAAGCT GTGCCACCCC GAGGAGCTGG TGCTGCTCGG ACACTCTCTG
601  GGCATCCCCT GGGCTCCCCT GAGCTCCTGC CCCAGCCAGG CCCTGCAGCT
651  GGCAGGCTGC TTGAGCCAAC TCCATAGCGG CCTTTTCCTC TACCAGGGGC
701  TCCTGCAGGC CCTGGAAGGG ATATCCCCCG AGTTGGGTCC CACCTTGGAC
751  ACACTGCAGC TGGACGTCGC CGACTTTGCC ACCACCATCT GGCAGCAGAT
801  GGAAGAACTG GGAATGGCCC CTGCCCTGCA GCCCACCCAG GGTGCCATGC
851  CGGCCTTCGC CTCTGCTTTC CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT
901  AGCCATCTGC AGAGCTTCCT GGAGGTGTCG TACCGCGTTC TACGCCACCT
951  TGCGCAGCCC GACATGGCTA CACCA (SEQ ID NO:259)
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pmon16018.seq

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  1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
 51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
101  CTATCCTGAT GGATCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTCAGAGC
451  TTCCTGCTCA AGTCTTTAGA GCAAGTGAGG AAGATCCAGG GCGATGGCGC
501  AGCGCTCCAG GAGAAGCTGT GTGCCACCTA CAAGCTGTGC CACCCCGAGG
551  AGCTGGTGCT GCTCGGACAC TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC
601  TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA GGCTGCTTGA GCCAACTCCA
651  TAGCGGCCTT TTCCTCTACC AGGGGCTCCT GCAGGCCCTG GAAGGGATAT
701  CCCCCGAGTT GGGTCCCACC TTGGACACAC TGCAGCTGGA CGTCGCCGAC
751  TTTGCCACCA CCATCTGGCA GCAGATGGAA GAACTGGGAA TGGCCCCTGC
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 801  CCTGCAGCCC ACCCAGGGTG CCATGCCGGC CTTCGCCTCT GCTTTCCAGC
 851  GCCGGGCAGG AGGGGTCCTG GTTGCTAGCC ATCTGCAGAG CTTCCTGGAG
 901  GTGTCGTACC GCGTTCTACG CCACCTTGCG CAGCCCGACA TGGCTACACC
 951  ATTAGGCCCT GCCAGCTCCC TGCCC (SEQ ID NO:260)
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pmon16019.seq

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   1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
  51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 101  CTATCCTGAT GGATCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
 151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
 401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTTTCCTG
 451  CTCAAGTCTT TAGAGCAAGT GAGGAAGATC CAGGGCGATG GCGCAGCGCT
 501  CCAGGAGAAG CTGTGTGCCA CCTACAAGCT GTGCCACCCC GAGGAGCTGG
 551  TGCTGCTCGG ACACTCTCTG GGCATCCCCT GGGCTCCCCT GAGCTCCTGC
 601  CCCAGCCAGG CCCTGCAGCT GGCAGGCTGC TTGAGCCAAC TCCATAGCGG
 651  CCTTTTCCTC TACCAGGGGC TCCTGCAGGC CCTGGAAGGG ATATCCCCCG
 701  AGTTGGGTCC CACCTTGGAC ACACTGCAGC TGGACGTCGC CGACTTTGCC
 751  ACCACCATCT GGCAGCAGAT GGAAGAACTG GGAATGGCCC CTGCCCTGCA
 801  GCCCACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC CAGCGCCGGG
 851  CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG
 901  TACCGCGTTC TACGCCACCT TGCGCAGCCC GACATGGCTA CACCATTAGG
 951  CCCTGCCAGC TCCCTGCCCC AGAGC (SEQ ID NO:261)
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pmon16020.seq

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   1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
  51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 101  CTATCCTGAT GGATCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
 151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
 401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTGAGCAA
 451  GTGAGGAAGA TCCAGGGCGA TGGCGCAGCG CTCCAGGAGA AGCTGTGTGC
 501  CACCTACAAG CTGTGCCACC CCGAGGAGCT GGTGCTGCTC GGACACTCTC
 551  TGGGCATCCC CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG
 601  CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCCTTTTCC TCTACCAGGG
 651  GCTCCTGCAG GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG
 701  ACACACTGCA GCTGGACGTC GCCGACTTTG CCACCACCAT CTGGCAGCAG
 751  ATGGAAGAAC TGGGAATGGC CCCTGCCCTG CAGCCCACCC AGGGTGCCAT
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 801  GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG GTCCTGGTTG
 851  CTAGCCATCT GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC
 901  CTTGCGCAGC CCGACATGGC TACACCATTA GGCCCTGCCA GCTCCCTGCC
 951  CCAGAGCTTC CTGCTCAAGT CTTTA (SEQ ID NO:262)
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pmon16021.seq

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   1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
  51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 101  CTATCCTGAT GGATCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
 151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
 401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTCTGCTC
 451  GGACACTCTC TGGGCATCCC CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA
 501  GGCCCTGCAG CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCCTTTTCC
 551  TCTACCAGGG GCTCCTGCAG GCCCTGGAAG GGATATCCCC CGAGTTGGGT
 601  CCCACCTTGG ACACACTGCA GCTGGACGTC GCCGACTTTG CCACCACCAT
 651  CTGGCAGCAG ATGGAAGAAC TGGGAATGGC CCCTGCCCTG CAGCCCACCC
 701  AGGGTGCCAT GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG
 751  GTCCTGGTTG CTAGCCATCT GCAGAGCTTC CTGGAGGTGT CGTACCGCGT
 801  TCTACGCCAC CTTGCGCAGC CCGACATGGC TACACCATTA GGCCCTGCCA
 851  GCTCCCTGCC CCAGAGCTTC CTGCTCAAGT CTTTAGAGCA AGTGAGGAAG
 901  ATCCAGGGCG ATGGCGCAGC GCTCCAGGAG AAGCTGTGTG CCACCTACAA
 951  GCTGTGCCAC CCCGAGGAGC TGGTG (SEQ ID NO:263)
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pmon16022.seq

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   1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
  51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 101  CTATCCTGAT GGATCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
 151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
 401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTCCCCTG
 451  AGCTCCTGCC CCAGCCAGGC CCTGCAGCTG GCAGGCTGCT TGAGCCAACT
 501  CCATAGCGGC CTTTTCCTCT ACCAGGGGCT CCTGCAGGCC CTGGAAGGGA
 551  TATCCCCCGA GTTGGGTCCC ACCTTGGACA CACTGCAGCT GGACGTCGCC
 601  GACTTTGCCA CCACCATCTG GCAGCAGATG GAAGAACTGG GAATGGCCCC
 651  TGCCCTGCAG CCCACCCAGG GTGCCATGCC GGCCTTCGCC TCTGCTTTCC
 701  AGCGCCGGGC AGGAGGGGTC CTGGTTGCTA GCCATCTGCA GAGCTTCCTG
 751  GAGGTGTCGT ACCGCGTTCT ACGCCACCTT GCGCAGCCCG ACATGGCTAC
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 801  ACCATTAGGC CCTGCCAGCT CCCTGCCCCA GAGCTTCCTG CTCAAGTCTT
 851  TAGAGCAAGT GAGGAAGATC CAGGGCGATG GCGCAGCGCT CCAGGAGAAG
 901  CTGTGTGCCA CCTACAAGCT GTGCCACCCC GAGGAGCTGG TGCTGCTCGG
 951  ACACTCTCTG GGCATCCCCT GGGCT (SEQ ID NO:264)
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pmon16023.seq

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   1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
  51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 101  CTATCCTGAT GGATCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
 151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
 401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTCAGGCC
 451  CTGCAGCTGG CAGGCTGCTT GAGCCAACTC CATAGCGGCC TTTTCCTCTA
 501  CCAGGGGCTC CTGCAGGCCC TGGAAGGGAT ATCCCCCGAG TTGGGTCCCA
 551  CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG
 601  CAGCAGATGG AAGAACTGGG AATGGCCCCT GCCCTGCAGC CCACCCAGGG
 651  TGCCATGCCG GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC
 701  TGGTTGCTAG CCATCTGCAG AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA
 751  CGCCACCTTG CGCAGCCCGA CATGGCTACA CCATTAGGCC CTGCCAGCTC
 801  CCTGCCCCAG AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG AGGAAGATCC
 851  AGGGCGATGG CGCAGCGCTC CAGGAGAAGC TGTGTGCCAC CTACAAGCTG
 901  TGCCACCCCG AGGAGCTGGT GCTGCTCGGA CACTCTCTGG GCATCCCCTG
 951  GGCTCCCCTG AGCTCCTGCC CCAGC (SEQ ID NO:265)
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pmon16024.seq

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   1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
  51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 101  CTATCCTGAT GGATCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
 151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
 401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTCTGCAG
 451  CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCCTTTTCC TCTACCAGGG
 501  GCTCCTGCAG GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG
 551  ACACACTGCA GCTGGACGTC GCCGACTTTG CCACCACCAT CTGGCAGCAG
 601  ATGGAAGAAC TGGGAATGGC CCCTGCCCTG CAGCCCACCC AGGGTGCCAT
 651  GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG GTCCTGGTTG
 701  CTAGCCATCT GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC
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  751  CTTGCGCAGC CCGACATGGC TACACCATTA GGCCCTGCCA GCTCCCTGCC
  801  CCAGAGCTTC CTGCTCAAGT CTTTAGAGCA AGTGAGGAAG ATCCAGGGCG
  851  ATGGCGCAGC GCTCCAGGAG AAGCTGTGTG CCACCTACAA GCTGTGCCAC
  901  CCCGAGGAGC TGGTGCTGCT CGGACACTCT CTGGGCATCC CCTGGGCTCC
  951  CCTGAGCTCC TGCCCCAGCC AGGCC (SEQ ID NO:266)
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pmon16025.seq

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    1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
   51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
  101  CTATCCTGAT GGATCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
  151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
  201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
  251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
  301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
  351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
  401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTCTGGCA
  451  GGCTGCTTGA GCCAACTCCA TAGCGGCCTT TTCCTCTACC AGGGGCTCCT
  501  GCAGGCCCTG GAAGGGATAT CCCCCGAGTT GGGTCCCACC TTGGACACAC
  551  TGCAGCTGGA CGTCGCCGAC TTTGCCACCA CCATCTGGCA GCAGATGGAA
  601  GAACTGGGAA TGGCCCCTGC CCTGCAGCCC ACCCAGGGTG CCATGCCGGC
  651  CTTCGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG GTTGCTAGCC
  701  ATCTGCAGAG CTTCCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG
  751  CAGCCCGACA TGGCTACACC ATTAGGCCCT GCCAGCTCCC TGCCCCAGAG
  801  CTTCCTGCTC AAGTCTTTAG AGCAAGTGAG GAAGATCCAG GGCGATGGCG
  851  CAGCGCTCCA GGAGAAGCTG TGTGCCACCT ACAAGCTGTG CCACCCCGAG
  901  GAGCTGGTGC TGCTCGGACA CTCTCTGGGC ATCCCCTGGG CTCCCCTGAG
  951  CTCCTGCCCC AGCCAGGCCC TGCAG (SEQ ID NO:267)
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pmon16026.seq

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    1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
   51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
  101  CTATCCTGAT GGATCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
  151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
  201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
  251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
  301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
  351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
  401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTGAACTG
  451  GGAATGGCCC CTGCCCTGCA GCCCACCCAG GGTGCCATGC CGGCCTTCGC
  501  CTCTGCTTTC CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC
  551  AGAGCTTCCT GGAGGTGTCG TACCGCGTTC TACGCCACCT TGCGCAGCCC
  601  GACATGGCTA CACCATTAGG CCCTGCCAGC TCCCTGCCCC AGAGCTTCCT
  651  GCTCAAGTCT TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT GGCGCAGCGC
  701  TCCAGGAGAA GCTGTGTGCC ACCTACAAGC TGTGCCACCC CGAGGAGCTG
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 751  GTGCTGCTCG GACACTCTCT GGGCATCCCC TGGGCTCCCC TGAGCTCCTG
 801  CCCCAGCCAG GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA CTCCATAGCG
 851  GCCTTTTCCT CTACCAGGGG CTCCTGCAGG CCCTGGAAGG GATATCCCCC
 901  GAGTTGGGTC CCACCTTGGA CACACTGCAG CTGGACGTCG CCGACTTTGC
 951  CACCACCATC TGGCAGCAGA TGGAA (SEQ ID NO:268)
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pmon16027.seq

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   1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
  51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 101  CTATCCTGAT GGATCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
 151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
 401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTGGAATG
 451  GCCCCTGCCC TGCAGCCCAC CCAGGGTGCC ATGCCGGCCT TCGCCTCTGC
 501  TTTCCAGCGC CGGGCAGGAG GGGTCCTGGT TGCTAGCCAT CTGCAGAGCT
 551  TCCTGGAGGT GTCGTACCGC GTTCTACGCC ACCTTGCGCA GCCCGACATG
 601  GCTACACCAT TAGGCCCTGC CAGCTCCCTG CCCCAGAGCT TCCTGCTCAA
 651  GTCTTTAGAG CAAGTGAGGA AGATCCAGGG CGATGGCGCA GCGCTCCAGG
 701  AGAAGCTGTG TGCCACCTAC AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG
 751  CTCGGACACT CTCTGGGCAT CCCCTGGGCT CCCCTGAGCT CCTGCCCCAG
 801  CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG CCAACTCCAT AGCGGCCTTT
 851  TCCTCTACCA GGGGCTCCTG CAGGCCCTGG AAGGGATATC CCCCGAGTTG
 901  GGTCCCACCT TGGACACACT GCAGCTGGAC GTCGCCGACT TTGCCACCAC
 951  CATCTGGCAG CAGATGGAAG AACTG (SEQ ID NO:269)
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pmon16028.seq

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   1  ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
  51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 101  CTATCCTGAT GGATCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
 151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
 401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTAGCTTC
 451  CTGGAGGTGT CGTACCGCGT TCTACGCCAC CTTGCGCAGC CCGACATGGC
 501  TACACCATTA GGCCCTGCCA GCTCCCTGCC CCAGAGCTTC CTGCTCAAGT
 551  CTTTAGAGCA AGTGAGGAAG ATCCAGGGCG ATGGCGCAGC GCTCCAGGAG
 601  AAGCTGTGTG CCACCTACAA GCTGTGCCAC CCCGAGGAGC TGGTGCTGCT
 651  CGGACACTCT CTGGGCATCC CCTGGGCTCC CCTGAGCTCC TGCCCCAGCC
```

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 701  AGGCCCTGCA GCTGGCAGGC TGCTTGAGCC AACTCCATAG CGGCCTTTTC
 751  CTCTACCAGG GGCTCCTGCA GGCCCTGGAA GGGATATCCC CCGAGTTGGG
 801  TCCCACCTTG GACACACTGC AGCTGGACGT CGCCGACTTT GCCACCACCA
 851  TCTGGCAGCA GATGGAAGAA CTGGGAATGG CCCCTGCCCT GCAGCCCACC
 901  CAGGGTGCCA TGCCGGCCTT CGCCTCTGCT TTCCAGCGCC GGGCAGGAGG
 951  GGTCCTGGTT GCTAGCCATC TGCAG (SEQ ID NO:270)

   1  ATGGCTGGAC CCACTTGCCT CTCATCCCTC CTGGGGCAGC TTTCTGGACA
  51  GGTCCGTCTC CTCCTTGGGG CCCTGCAGAG CCTCCTTGGA ACCCAGCTTC
 101  CTCCACAGGG CAGGACCACA GCTCACAAGG ATCCCAATGC CATCTTCCTG
 151  AGCTTCCAAC ACCTGCTCCG AGGAAAGGTG CGTTTCCTGA TGCTTGTAGG
 201  AGGGTCCACC CTCGCCGTCA GGGAATTCGG CGGCAACATG GCGTCTCCGG
 251  CGCCGCCTGC TGCTGACCTC CGAGTCCTCA GTAAACTGCT TCGTGACTCC
 301  CATGTCCTTC ACAGCAGACT GAGCCAGTGC CCAGAGGTTC ACCCTTTGCC
 351  TACACCTGTC CTGCTGCCTG CTGTGGACTT TAGCTTGGGA GAATGGAAAA
 401  CCCAGATGGA GGAGACCAAG GCACAGGACA TTCTGGGAGC AGTGACCCTT
 451  CTGCTGGAGG GAGTGATGGC AGCACGGGGA CAACTG
      (SEQ ID NO:286)

   1  ATGGCTGGCA GGACCACAGC TCACAAGGAT CCCAATGCCA TCTTCCTGAG
  51  CTTCCAACAC CTGCTCCGAG GAAAGGTGCG TTTCCTGATG CTTGTAGGAG
 101  GGTCCACCCT CGCCGTCAGG GAATTCGGCG GCAACATGGC GTCTCCGGCG
 151  CCGCCTGCTG CTGACCTCCG AGTCCTCAGT AAACTGCTTC GTGACTCCCA
 201  TGTCCTTCAC AGCAGACTGA GCCAGTGCCC AGAGGTTCAC CCTTTGCCTA
 251  CACCTGTCCT GCTGCCTGCT GTGGACTTTA GCTTGGGAGA ATGGAAAACC
 301  CAGATGGAGG AGACCAAGGC ACAGGACATT CTGGGAGCAG TGACCCTTCT
 351  GCTGGAGGGA GTGATGGCAG CACGGGGACA ACTGGGACCC ACTTGCCTCT
 401  CATCCCTCCT GGGGCAGCTT TCTGGACAGG TCCGTCTCCT CCTTGGGGCC
 451  CTGCAGAGCC TCCTTGGAAC CCAGCTTCCT CCACAG
      (SEQ ID NO:287)
```

TABLE 3

PROTEIN SEQUENCES

pMON26458pep

SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHis
ValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeu
LeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAla
GlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGln
LeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeu
LeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThrAla
HisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArg
PheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPhe
(SEQ ID NO:161)

pMON28548pep

SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHis
ValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeu
LeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAla
GlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGln
LeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeu
LeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThrAla
HisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArg
PheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGlyGlyAsnMetAla
SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHis
ValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeu
LeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAla
GlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGln
LeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeu
LeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnGlyArgThrThrAlaHisLysAspPro
AsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPheLeuMetLeu
ValGlyGlySerThrLeuCysValArg (SEQ ID NO:162)

pMON28500

SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHisVa
lLeu
HisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeuLeuProAl
aVal
AspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGl
yAla
ValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSe
rSer
LeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGl
yThr

GlnLeuProProGlnGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPh
eGln
HisLeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysValAr
gGlu
PheGlyAsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLe
uArg
AspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrPr
oVal
LeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAl
aGln
AspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGl
yPro
ThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAlaLe
uGln
SerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLysAspProAsnAl
aIle
PheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySe
rThr
LeuCysValArg (SEQ ID NO:163)

pMON28501

SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHis
ValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeu
LeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAla
GlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGln
LeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeu
LeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThrAla
HisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArg
PheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGlyGlyAsnMetAla
SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHis
ValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeu
LeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAla
GlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGln
LeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeu
LeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThrAla
HisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArg
PheLeuMetLeuValGlyGlySerThrLeuCysValArg (SEQ ID NO:164)

pMON28502

SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHis
ValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeu
LeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAla
GlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGln
LeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeu
LeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThrAla

HisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArg
PheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGlyGlyAsnGlyGly
AsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArg
AspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThr
ProValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGlu
ThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAla
ArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnVal
ArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArg
ThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGly
LysValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArg
(SEQ ID NO:165)

13182.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Tyr Lys Leu Cys
His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro
Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala
Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly
Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr
Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile
Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg
Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser Gly Gly
Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val
Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys
Ala Thr (SEQ ID NO:166)

13183.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro

Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Tyr Lys Leu Cys
His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro
Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala
Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly
Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr
Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile
Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg
Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser Gly Gly
Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val
Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys
Ala Thr (SEQ ID NO:167)

13184.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Pro Glu Leu Gly
Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr
Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu
Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln
Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser
Gly Gly Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu
Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys
Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu
Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
Ile Ser (SEQ ID NO:168)

13185.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile

Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Pro Glu Leu Gly
Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr
Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu
Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln
Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser
Gly Gly Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu
Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys
Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu
Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
Ile Ser (SEQ ID NO:169)

13186.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Met Ala Pro Ala
Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
Ser Gly Gly Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu
Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu
Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu
His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu
Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu
Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu
Leu Gly (SEQ ID NO:170)

13187.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Met Ala Pro Ala
Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
Ser Gly Gly Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu
Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu
Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu
His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu
Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu
Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu
Leu Gly (SEQ ID NO:171)

13188.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Thr Gln Gly Ala
Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val
Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg
Val Leu Arg His Leu Ala Gln Pro Ser Gly Gly Ser Gly Gly Ser
Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln
Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys
Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly
Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln
Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr
Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly
Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr
Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu
Gln Pro (SEQ ID NO:172)

13189.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Thr Gln Gly Ala
Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val
Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg
Val Leu Arg His Leu Ala Gln Pro Ser Gly Gly Ser Gly Gly Ser
Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln
Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys
Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly
Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln
Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr
Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly
Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr
Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu
Gln Pro (SEQ ID NO:173)

13190.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Ser Ala Phe Gln
Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser
Gly Gly Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu
Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys
Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu
Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly

Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp
Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu
Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala
Phe Ala (SEQ ID NO:174)

13191.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Ser Ala Phe Gln
Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser
Gly Gly Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu
Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys
Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu
Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp
Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu
Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala
Phe Ala (SEQ ID NO:175)

13192.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Tyr Lys Leu Cys
His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro
Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala
Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly
Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr

Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile
Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg
Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Thr Pro Leu
Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu
Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu
Lys Leu Cys Ala Thr (SEQ ID NO:176)

13193.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Tyr Lys Leu Cys
His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro
Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala
Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly
Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr
Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile
Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg
Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Thr Pro Leu
Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu
Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu
Lys Leu Cys Ala Thr (SEQ ID NO:177)

25190.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Pro Glu Leu Gly

Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr
Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu
Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln
Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Thr
Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu
Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala
Leu Glu Gly Ile Ser (SEQ ID NO:178)

pMON25191.Pep

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Pro Glu Leu Gly
Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr
Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu
Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln
Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Thr
Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu
Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala
Leu Glu Gly Ile Ser (SEQ ID NO:179)

13194.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr

Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Met Ala Pro Ala
Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala
Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu
Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro
Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu
Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln
Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr
Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln
Met Glu Glu Leu Gly (SEQ ID NO:180)

13195.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Met Ala Pro Ala
Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala
Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu
Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro
Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu
Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln
Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr
Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln
Met Glu Glu Leu Gly (SEQ ID NO:181)

13196.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg

Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Thr Gln Gly Ala
Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val
Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg
Val Leu Arg His Leu Ala Gln Pro Thr Pro Leu Gly Pro Ala Ser
Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg
Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala
Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His
Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln
Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu
Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro
Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
Pro Ala Leu Gln Pro (SEQ ID NO:182)

13197.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Thr Gln Gly Ala
Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val
Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg
Val Leu Arg His Leu Ala Gln Pro Thr Pro Leu Gly Pro Ala Ser
Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg
Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala
Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His
Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln
Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu
Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro
Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
Pro Ala Leu Gln Pro (SEQ ID NO:183)

13198.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Ser Ala Phe Gln
Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Thr
Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu
Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala
Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu
Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met
Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala
Met Pro Ala Phe Ala (SEQ ID NO:184)

13199.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Ser Ala Phe Gln
Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Thr
Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu
Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala

Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu
Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met
Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala
Met Pro Ala Phe Ala (SEQ ID NO:185)

31104.Pep

Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val Ser Ile Leu Met
Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe Val Arg Ala
Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg
Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg
His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu
Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
Gln Gly Gly Gly Ser Asn Cys Ser Ile Met Ile Asp Glu Ile Ile
His His Leu Lys Arg Pro Pro Ala Pro Leu Tyr Val Glu Gly Gly
Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn
Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg
Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser Gly Gly
Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val
Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys
Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly
His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser
Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly
Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
Ala Pro Ala Leu Gln Pro (SEQ ID NO:186)

31105.Pep

Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys
Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile
Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr
Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln Gly Gly Gly Ser
Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Tyr Val Glu Gly Gly
Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn
Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg
Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser Gly Gly

Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val
Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys
Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly
His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser
Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly
Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
Ala Pro Ala Leu Gln Pro (SEQ ID NO:187)

31106.Pep

Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln
Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln
Ala Gln Glu Gln Gln Gly Gly Gly Ser Asn Cys Ser Ile Met Ile
Asp Glu Ile Ile His His Leu Lys Arg Pro Pro Ala Pro Leu Leu
Asp Pro Asn Asn Leu Asn Asp Glu Asp Val Ser Ile Leu Met Asp
Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe Val Arg Ala Val
Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg Asn
Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Tyr Val Glu Gly Gly
Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn
Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg
Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser Gly Gly
Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val
Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys
Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly
His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser
Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly
Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
Ala Pro Ala Leu Gln Pro (SEQ ID NO:188)

31107.Pep

Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu
Val Thr Leu Glu Gln Ala Gln Glu Gln Gln Gly Gly Gly Ser Asn
Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro
Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val
Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu
Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala
Ala Pro Ser Arg His Pro Ile Ile Ile Lys Tyr Val Glu Gly Gly

Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn
Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg
Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser Gly Gly
Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val
Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys
Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly
His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser
Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly
Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
Ala Pro Ala Leu Gln Pro (SEQ ID NO:189)

31108.Pep

Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val Ser Ile Leu Met
Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe Val Arg Ala
Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg
Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg
His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu
Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
Gln Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Asn Cys
Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro Pro
Ala Pro Leu Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro
Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu
Ser His Lys Ser Pro Asn Met Ala Thr Gln Gly Ala Met Pro Ala
Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala
Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg
His Leu Ala Gln Pro Ser Gly Gly Ser Gly Gly Ser Gln Ser Phe
Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly
Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His
Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp
Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly
Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu
Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu
Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp
Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
(SEQ ID NO:190)

31109.Pep

Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys
Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile
Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr

Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln Gly Gly Gly Ser
Gly Gly Gly Ser Gly Gly Gly Ser Asn Cys Ser Ile Met Ile Asp
Glu Ile Ile His His Leu Lys Arg Pro Pro Ala Pro Leu Leu Asp
Pro Asn Asn Leu Asn Asp Glu Asp Val Ser Ile Leu Met Asp Arg
Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe Val Arg Ala Val Lys
Asn Leu Glu Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro
Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu
Ser His Lys Ser Pro Asn Met Ala Thr Gln Gly Ala Met Pro Ala
Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala
Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg
His Leu Ala Gln Pro Ser Gly Gly Ser Gly Gly Ser Gln Ser Phe
Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly
Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His
Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp
Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly
Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu
Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu
Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp
Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
(SEQ ID NO:191)

31110.Pep

Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln
Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln
Ala Gln Glu Gln Gln Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
Gly Ser Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu
Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp
Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn
Leu Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser
Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser
Ala Thr Ala Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro
Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu
Ser His Lys Ser Pro Asn Met Ala Thr Gln Gly Ala Met Pro Ala
Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala
Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg
His Leu Ala Gln Pro Ser Gly Gly Ser Gly Gly Ser Gln Ser Phe
Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly
Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His
Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp
Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly
Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu
Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu
Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp
Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
(SEQ ID NO:192)

31111.Pep

Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu
Val Thr Leu Glu Gln Ala Gln Glu Gln Gln Gly Gly Gly Ser Gly
Gly Gly Ser Gly Gly Gly Ser Asn Cys Ser Ile Met Ile Asp Glu
Ile Ile His His Leu Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro
Asn Asn Leu Asn Asp Glu Asp Val Ser Ile Leu Met Asp Arg Asn
Leu Arg Leu Pro Asn Leu Glu Ser Phe Val Arg Ala Val Lys Asn
Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln
Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg His Pro Ile
Ile Ile Lys Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro
Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu
Ser His Lys Ser Pro Asn Met Ala Thr Gln Gly Ala Met Pro Ala
Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala
Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg
His Leu Ala Gln Pro Ser Gly Gly Ser Gly Gly Ser Gln Ser Phe
Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly
Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His
Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp
Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly
Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu
Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu
Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp
Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
(SEQ ID NO:193)

pMON15981

MetAlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAla
ProLeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsn
LeuArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSer
GlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaPro
SerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThr
PheTyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGly
SerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGlu
SerHisLysSerProAsnMetAlaTyrLysLeuCysHisProGluGluLeuValLeuLeu
GlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGln
LeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGln
AlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspVal
AlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeu
GlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGly
ValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHis
LeuAlaGlnProGlyGlyGlySerAspMetAlaThrProLeuGlyProAlaSerSerLeu
ProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAla
AlaLeuGlnGluLysLeuCysAlaThr (SEQ ID NO:194)

pMON15982

MetAlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAla
ProLeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsn
LeuArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSer
GlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaPro
SerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThr
PheTyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGly
SerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGlu
SerHisLysSerProAsnMetAlaProGluLeuGlyProThrLeuAspThrLeuGlnLeu
AspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaPro
AlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAla
GlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeu
ArgHisLeuAlaGlnProGlyGlyGlySerAspMetAlaThrProLeuGlyProAlaSer
SerLeuProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAsp
GlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeu
ValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGln
AlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGly
LeuLeuGlnAlaLeuGluGlyIleSer (SEQ ID NO:195)

pMON15965

MetAlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAla
ProLeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsn
LeuArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSer
GlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaPro
SerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThr
PheTyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGly
SerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGlu
SerHisLysSerProAsnMetAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuVal
AlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGln
ProGlyGlyGlySerAspMetAlaThrProLeuGlyProAlaSerSerLeuProGlnSer
PheLeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGln
GluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHis
SerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAla
GlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeu
GluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAsp
PheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeuGlnPro
ThrGlnGlyAlaMetProAlaPheAla (SEQ ID NO:196)

pMON15966

MetAlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAla
ProLeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsn
LeuArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSer
GlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaPro
SerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThr
PheTyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGly

SerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGlu
SerHisLysSerProAsnMetAlaMetAlaProAlaLeuGlnProThrGlnGlyAlaMet
ProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAlaSerHisLeu
GlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnProGlyGlyGly
SerAspMetAlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLys
SerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCys
AlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeuGlyIle
ProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSer
GlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSer
ProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThr
IleTrpGlnGlnMetGluGluLeuGly (SEQ ID NO:197)

pMON15967

MetAlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAla
ProLeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsn
LeuArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSer
GlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaPro
SerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThr
PheTyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGly
SerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGlu
SerHisLysSerProAsnMetAlaThrGlnGlyAlaMetProAlaPheAlaSerAlaPhe
GlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSer
TyrArgValLeuArgHisLeuAlaGlnProGlyGlyGlySerAspMetAlaThrProLeu
GlyProAlaSerSerLeuProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLys
IleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHis
ProGluGluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSer
CysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPhe
LeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeu
AspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGlu
LeuGlyMetAlaProAlaLeuGlnPro (SEQ ID NO:198)

pMON31112.pep

MetAlaAsnCysSerAsnMetIleAspGluIleIleThrHisLeuLysGlnProProLeu
ProLeuLeuAspPheAsnAsnLeuAsnGlyGluAspGlnAspIleLeuMetAspAsnAsn
LeuArgArgProAsnLeuGluAlaPheAsnArgAlaValLysSerLeuGlnAsnAlaSer
AlaIleGluSerIleLeuLysAsnLeuLeuProCysLeuProLeuAlaThrAlaAlaPro
ThrArgHisProIleHisIleLysAspGlyAspTrpAsnGluPheArgArgLysLeuThr
PheTyrLeuLysThrLeuGluAsnAlaGlnAlaGlnGlnTyrValGluGlyGlyGlyGly
SerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGlu
SerHisLysSerProAsnMetAlaThrGlnGlyAlaMetProAlaPheAlaSerAlaPhe
GlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSer
TyrArgValLeuArgHisLeuAlaGlnProSerGlyGlySerGlyGlySerGlnSerPhe
LeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGlu
LysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSer

LeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGly
CysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGlu
GlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPhe
AlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeuGlnPro
(SEQ ID NO:199)

pMON31113.pep

MetAlaAsnCysSerAsnMetIleAspGluIleIleThrHisLeuLysGlnProProLeu
ProLeuLeuAspPheAsnAsnLeuAsnGlyGluAspGlnAspIleLeuMetGluAsnAsn
LeuArgArgProAsnLeuGluAlaPheAsnArgAlaValLysSerLeuGlnAsnAlaSer
AlaIleGluSerIleLeuLysAsnLeuLeuProCysLeuProLeuAlaThrAlaAlaPro
ThrArgHisProIleIleIleArgAspGlyAspTrpAsnGluPheArgArgLysLeuThr
PheTyrLeuLysThrLeuGluAsnAlaGlnAlaGlnGlnTyrValGluGlyGlyGlyGly
SerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGlu
SerHisLysSerProAsnMetAlaThrGlnGlyAlaMetProAlaPheAlaSerAlaPhe
GlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSer
TyrArgValLeuArgHisLeuAlaGlnProThrProLeuGlyProAlaSerSerLeuPro
GlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAla
LeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeu
GlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGln
LeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGln
AlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspVal
AlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeu
GlnPro (SEQ ID NO:200)

pMON31114.pep

MetAlaAsnCysSerAsnMetIleAspGluIleIleThrHisLeuLysGlnProProLeu
ProLeuLeuAspPheAsnAsnLeuAsnGlyGluAspGlnAspIleLeuMetGluAsnAsn
LeuArgArgProAsnLeuGluAlaPheAsnArgAlaValLysSerLeuGlnAsnAlaSer
AlaIleGluSerIleLeuLysAsnLeuLeuProCysLeuProLeuAlaThrAlaAlaPro
ThrArgHisProIleIleIleArgAspGlyAspTrpAsnGluPheArgArgLysLeuThr
PheTyrLeuLysThrLeuGluAsnAlaGlnAlaGlnGlnTyrValGluGlyGlyGlyGly
SerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGlu
SerHisLysSerProAsnMetAlaThrGlnGlyAlaMetProAlaPheAlaSerAlaPhe
GlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSer
TyrArgValLeuArgHisLeuAlaGlnProSerGlyGlySerGlyGlySerGlnSerPhe
LeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGlu
LysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSer
LeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGly
CysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGlu
GlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPhe
AlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeuGlnPro
(SEQ ID NO:201)

pMON31115.pep

MetAlaAsnCysSerAsnMetIleAspGluIleIleThrHisLeuLysGlnProProLeu
ProLeuLeuAspPheAsnAsnLeuAsnGlyGluAspGlnAspIleLeuMetAspAsnAsn
LeuArgArgProAsnLeuGluAlaPheAsnArgAlaValLysSerLeuGlnAsnAlaSer
AlaIleGluSerIleLeuLysAsnLeuLeuProCysLeuProLeuAlaThrAlaAlaPro
ThrArgHisProIleHisIleLysAspGlyAspTrpAsnGluPheArgArgLysLeuThr
PheTyrLeuLysThrLeuGluAsnAlaGlnAlaGlnGlnTyrValGluGlyGlyGlyGly
SerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGlu
SerHisLysSerProAsnMetAlaThrGlnGlyAlaMetProAlaPheAlaSerAlaPhe
GlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSer
TyrArgValLeuArgHisLeuAlaGlnProThrProLeuGlyProAlaSerSerLeuPro
GlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAla
LeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeu
GlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGln
LeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGln
AlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspVal
AlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeu
GlnPro (SEQ ID NO:202)

pMON28505

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetGluValHisProLeuProThrProValLeuLeuProAlaVal
AspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeu
GlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProThr
CysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeu
GlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLysAspPro
AsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPheLeuMetLeu
ValGlyGlySerThrLeuCysValArgGluPheGlyGlyAsnMetAlaSerProAlaPro
ProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHisValLeuHisSer
ArgLeuSerGlnCysPro (SEQ ID NO:203)

pMON28506

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly

IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetLeuProThrProValLeuLeuProAlaValAspPheSerLeu
GlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThr
LeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSer
LeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeu
GlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLysAspProAsnAlaIlePhe
LeuSerPheGlnHisLeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySer
ThrLeuCysValArgGluPheGlyGlyAsnMetAlaSerProAlaProProAlaCysAsp
LeuArgValLeuSerLysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGln
CysProGluValHisPro (SEQ ID NO:204)

pMON28507

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLys
ThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGlu
GlyValMetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGln
LeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeu
ProProGlnGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGln
HisLeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysVal
ArgGluPheGlyGlyAsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeu
SerLysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluVal
HisProLeuProThrPro (SEQ ID NO:205)

pMON28508

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGlu
GluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAla
AlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGln
ValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGly
ArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArg

GlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGly
GlyAsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeu
ArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuPro
ThrProValLeuLeuPro (SEQ ID NO:206)

pMON28509

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThr
LysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArg
GlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArg
LeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThr
ThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLys
ValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGlyGlyAsn
MetAlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAsp
SerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrPro
ValLeuLeuProAlaVal (SEQ ID NO:207)

pMON28510

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAsp
IleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGly
ProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGly
AlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLys
AspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPheLeu
MetLeuValGlyGlySerThrLeuCysValArgGluPheGlyGlyAsnMetAlaSerPro
AlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHisValLeu
HisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeuLeuPro
AlaValAspPheSerLeu (SEQ ID NO:208)

pMON28511

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu

ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGly
GlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGln
GlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeu
ArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPhe
GlyGlyAsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeu
LeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeu
ProThrProValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMet
GluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMet
AlaAlaArgGlyGlnLeu (SEQ ID NO:209)

pMON28512

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetGlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLys
AspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPheLeu
MetLeuValGlyGlySerThrLeuCysValArgGluPheGlyGlyAsnMetAlaSerPro
AlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHisValLeu
HisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeuLeuPro
AlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAsp
IleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGly
ProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGly
AlaLeuGlnSerLeuLeu (SEQ ID NO:210)

pMON28513

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeu
SerPheGlnHisLeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThr
LeuCysValArgGluPheGlyGlyAsnMetAlaSerProAlaProProAlaCysAspLeu
ArgValLeuSerLysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCys

ProGluValHisProLeuProThrProValLeuLeuProAlaValAspPheSerLeuGly
GluTrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeu
LeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeu
LeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGly
ThrGlnLeuProProGln (SEQ ID NO:211)

pMON28514

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHis
LeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArg
GluPheGlyGlyAsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSer
LysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHis
ProLeuProThrProValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThr
GlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGly
ValMetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeu
SerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuPro
ProGlnGlyArgThrThr (SEQ ID NO:212)

pMON28515

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArg
GlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGly
GlyAsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeu
ArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuPro
ThrProValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGlu
GluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAla
AlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGln
ValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGly
ArgThrThrAlaHisLys (SEQ ID NO:213)

pMON28516

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro

LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysVal
ArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGlyGlyAsnMet
AlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSer
HisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProVal
LeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLys
AlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGly
GlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeu
LeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThr
AlaHisLysAspProAsn (SEQ ID NO:214)

pMON28519

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetGluValHisProLeuProThrProValLeuLeuProAlaVal
AspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeu
GlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProThr
CysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeu
GlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLysAspPro
AsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPheLeuMetLeu
ValGlyGlySerThrLeuCysValArgGluPheGlyAsnMetAlaSerProAlaProPro
AlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHisValLeuHisSerArg
LeuSerGlnCysPro (SEQ ID NO:215)

pMON28520

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetLeuProThrProValLeuLeuProAlaValAspPheSerLeu
GlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThr
LeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSer

LeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeu
GlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLysAspProAsnAlaIlePhe
LeuSerPheGlnHisLeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySer
ThrLeuCysValArgGluPheGlyAsnMetAlaSerProAlaProProAlaCysAspLeu
ArgValLeuSerLysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCys
ProGluValHisPro (SEQ ID NO:216)

pMON28521

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLys
ThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGlu
GlyValMetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGln
LeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeu
ProProGlnGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGln
HisLeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysVal
ArgGluPheGlyAsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSer
LysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHis
ProLeuProThrPro (SEQ ID NO:217)

pMON28522

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGlu
GluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAla
AlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGln
ValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGly
ArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArg
GlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGly
AsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArg
AspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThr
ProValLeuLeuPro (SEQ ID NO:218)

pMON28523

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThr
LysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArg
GlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArg
LeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThr
ThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLys
ValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGlyAsnMet
AlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSer
HisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProVal
LeuLeuProAlaVal (SEQ ID NO:219)

pMON28524

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAsp
IleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGly
ProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGly
AlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLys
AspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPheLeu
MetLeuValGlyGlySerThrLeuCysValArgGluPheGlyAsnMetAlaSerProAla
ProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHisValLeuHis
SerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeuLeuProAla
ValAspPheSerLeu (SEQ ID NO:220)

pMON28525

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGly
GlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGln

GlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeu
ArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPhe
GlyAsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeu
ArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuPro
ThrProValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGlu
GluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAla
AlaArgGlyGlnLeu (SEQ ID NO:221)

pMON28526

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetGlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLys
AspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPheLeu
MetLeuValGlyGlySerThrLeuCysValArgGluPheGlyAsnMetAlaSerProAla
ProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHisValLeuHis
SerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeuLeuProAla
ValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAspIle
LeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyPro
ThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAla
LeuGlnSerLeuLeu (SEQ ID NO:222)

pMON28527

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeu
SerPheGlnHisLeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThr
LeuCysValArgGluPheGlyAsnMetAlaSerProAlaProProAlaCysAspLeuArg
ValLeuSerLysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysPro
GluValHisProLeuProThrProValLeuLeuProAlaValAspPheSerLeuGlyGlu
TrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeu
LeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeu
GlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThr
GlnLeuProProGln (SEQ ID NO:223)

pMON28528

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHis
LeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArg
GluPheGlyAsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSerLys
LeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisPro
LeuProThrProValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGln
MetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyVal
MetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSer
GlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProPro
GlnGlyArgThrThr (SEQ ID NO:224)

pMON28529

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArg
GlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGly
AsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArg
AspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThr
ProValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGlu
ThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAla
ArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnVal
ArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArg
ThrThrAlaHisLys (SEQ ID NO:225)

pMON28530

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysVal

ArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGlyAsnMetAla
SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHis
ValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeu
LeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAla
GlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGln
LeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeu
LeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThrAla
HisLysAspProAsn (SEQ ID NO:226)

pMON28533

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetGluValHisProLeuProThrProValLeuLeuProAlaVal
AspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeu
GlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProThr
CysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeu
GlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLysAspPro
AsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPheLeuMetLeu
ValGlyGlySerThrLeuCysValArgGluPheGlyGlyAsnGlyGlyAsnMetAlaSer
ProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHisVal
LeuHisSerArgLeuSerGlnCysPro (SEQ ID NO:227)

pMON28534

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetLeuProThrProValLeuLeuProAlaValAspPheSerLeu
GlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThr
LeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSer
LeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeu
GlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLysAspProAsnAlaIlePhe
LeuSerPheGlnHisLeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySer
ThrLeuCysValArgGluPheGlyGlyAsnGlyGlyAsnMetAlaSerProAlaProPro
AlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHisValLeuHisSerArg
LeuSerGlnCysProGluValHisPro (SEQ ID NO:228)

pMON28535

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLys
ThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGlu
GlyValMetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGln
LeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeu
ProProGlnGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGln
HisLeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysVal
ArgGluPheGlyGlyAsnGlyGlyAsnMetAlaSerProAlaProProAlaCysAspLeu
ArgValLeuSerLysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCys
ProGluValHisProLeuProThrPro (SEQ ID NO:229)

pMON28536

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGlu
GluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAla
AlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGln
ValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGly
ArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArg
GlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGly
GlyAsnGlyGlyAsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSer
LysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHis
ProLeuProThrProValLeuLeuPro (SEQ ID NO:230)

pMON28537

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer

HisLysSerProAsnMetAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThr
LysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArg
GlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArg
LeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThr
ThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLys
ValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGlyGlyAsn
GlyGlyAsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeu
LeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeu
ProThrProValLeuLeuProAlaVal (SEQ ID NO:231)

pMON28538

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAsp
IleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGly
ProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGly
AlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLys
AspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPheLeu
MetLeuValGlyGlySerThrLeuCysValArgGluPheGlyGlyAsnGlyGlyAsnMet
AlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSer
HisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProVal
LeuLeuProAlaValAspPheSerLeu (SEQ ID NO:232)

pMON28539

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGly
GlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGln
GlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeu
ArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPhe
GlyGlyAsnGlyGlyAsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeu
SerLysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluVal
HisProLeuProThrProValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLys
ThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGlu
GlyValMetAlaAlaArgGlyGlnLeu (SEQ ID NO:233)

pMON28540

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetGlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLys
AspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPheLeu
MetLeuValGlyGlySerThrLeuCysValArgGluPheGlyGlyAsnGlyGlyAsnMet
AlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSer
HisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProVal
LeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLys
AlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGly
GlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeu
LeuLeuGlyAlaLeuGlnSerLeuLeu (SEQ ID NO:234)

pMON28541

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeu
SerPheGlnHisLeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThr
LeuCysValArgGluPheGlyGlyAsnGlyGlyAsnMetAlaSerProAlaProProAla
CysAspLeuArgValLeuSerLysLeuLeuArgAspSerHisValLeuHisSerArgLeu
SerGlnCysProGluValHisProLeuProThrProValLeuLeuProAlaValAspPhe
SerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAla
ValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProThrCysLeu
SerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSer
LeuLeuGlyThrGlnLeuProProGln (SEQ ID NO:235)

pMON28542

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer

ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHis
LeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArg
GluPheGlyGlyAsnGlyGlyAsnMetAlaSerProAlaProProAlaCysAspLeuArg
ValLeuSerLysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysPro
GluValHisProLeuProThrProValLeuLeuProAlaValAspPheSerLeuGlyGlu
TrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeu
LeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeu
GlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThr
GlnLeuProProGlnGlyArgThrThr (SEQ ID NO:236)

pMON28543

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArg
GlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGly
GlyAsnGlyGlyAsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSer
LysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHis
ProLeuProThrProValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThr
GlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGly
ValMetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeu
SerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuPro
ProGlnGlyArgThrThrAlaHisLys (SEQ ID NO:237)

pMON28544

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysVal
ArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGlyGlyAsnGly
GlyAsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeu
ArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuPro
ThrProValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGlu
GluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAla
AlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGln
ValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGly

ArgThrThrAlaHisLysAspProAsn (SEQ ID NO:238)

pMON28545

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArg
GlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGly
GlyAsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeu
ArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuPro
ThrProValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGlu
GluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAla
AlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGln
ValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnGlyArgThrThrAla
HisLys (SEQ ID NO:239)

pMON32132

SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHis
ValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeu
LeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAla
GlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGln
LeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeu
LeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThrAla
HisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArg
PheLeuMetLeuValGlyGlySerThrLeuCysValArg (SEQ ID NO:252)

PMON32133

SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHis
ValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeu
LeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAla
GlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGln
LeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeu
LeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnGlyArgThrThrAlaHisLysAspPro
AsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPheLeuMetLeu
ValGlyGlySerThrLeuCysValArg (SEQ ID NO:253)

PMON32134

SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHis
ValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeu
LeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAla
GlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGln
LeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeu
LeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThrAla
HisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArg
PheLeuMetLeuValGlyGlySerThrLeuCysValArg (SEQ ID NO:254)

pmon16017.pep

1 Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu
16 Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp
31 Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn
46 Leu Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser
61 Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser
76 Ala Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly
91 Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr
106 Leu Glu Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly
121 Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser
136 Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Leu Gly
151 Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu Glu
166 Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys
181 Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu
196 Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
211 Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
226 Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
241 Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp

256 Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu
Leu
271 Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro
Ala
286 Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val
Ala
301 Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu
Arg
316 His Leu Ala Gln Pro Asp Met Ala Thr Pro (SEQ ID NO:271)

pmon16018.pep

1 Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
Leu
16 Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn
Asp
31 Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro
Asn
46 Leu Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala
Ser
61 Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro
Ser
76 Ala Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala
Gly
31 Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val
Thr
106 Leu Glu Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly
Gly
121 Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro
Ser
136 Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Leu
Gly
151 Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu
Glu
176 Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu
Lys
191 Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
Leu
206 Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
Cys
221 Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu
His
236 Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu
Gly
251 Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu
Asp

266 Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu
Leu
281 Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro
Ala
296 Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val
Ala
311 Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu
Arg
326 His Leu Ala Gln Pro Asp Met Ala Thr Pro (SEQ ID NO:272)

pmon16019.pep

1 Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
Leu
16 Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn
Asp
31 Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro
Asn
46 Leu Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala
Ser
61 Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro
Ser
76 Ala Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala
Gly
91 Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val
Thr
106 Leu Glu Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly
Gly
121 Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro
Ser
136 Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Phe
Leu
151 Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly
Ala
166 Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His
Pro
181 Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp
Ala
196 Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly
Cys
211 Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu
Leu
226 Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu
Asp
241 Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp
Gln

256 Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln
271 Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly
286 Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser
301 Tyr Arg Val Leu Arg His Leu Ala Gln Pro Asp Met Ala Thr Pro
316 Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser (SEQ ID NO:273)

pmon16020.pep

1 Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu
16 Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp
31 Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn
46 Leu Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser
61 Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser
76 Ala Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly
91 Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr
106 Leu Glu Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly
121 Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser
136 Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Glu Gln
151 Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu
166 Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu
181 Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro
196 Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
211 Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
226 Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val
241 Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly

256 Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe
271 Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser
286 His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His
301 Leu Ala Gln Pro Asp Met Ala Thr Pro Leu Gly Pro Ala Ser Ser
316 Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu (SEQ ID NO:274)

pmon16021.pep

1 Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu
16 Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp
31 Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn
46 Leu Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser
61 Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser
76 Ala Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly
91 Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr
106 Leu Glu Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly
121 Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser
136 Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Leu Leu
151 Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro
166 Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
181 Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
196 Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val
211 Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly
226 Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe
241 Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser

256 His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg
His
271 Leu Ala Gln Pro Asp Met Ala Thr Pro Leu Gly Pro Ala Ser
Ser
286 Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg
Lys
301 Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala
Thr
316 Tyr Lys Leu Cys His Pro Glu Glu Leu Val (SEQ ID NO:275)

pmon16022.pep

1 Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
Leu
16 Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn
Asp
31 Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro
Asn
46 Leu Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala
Ser
61 Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro
Ser
76 Ala Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala
Gly
91 Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val
Thr
106 Leu Glu Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly
Gly
121 Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro
Ser
136 Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Pro
Leu
151 Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu
Ser
166 Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln
Ala
181 Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr
Leu
196 Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln
Met
211 Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly
Ala
226 Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly
Val
241 Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr
Arg

256 Val Leu Arg His Leu Ala Gln Pro Asp Met Ala Thr Pro Leu Gly
271 Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu Glu
286 Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys
301 Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu
316 Leu Gly His Ser Leu Gly Ile Pro Trp Ala (SEQ ID NO:276)

pmon16023.pep

1 Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu
16 Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp
31 Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn
46 Leu Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser
61 Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser
76 Ala Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly
91 Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr
106 Leu Glu Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly
121 Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser
136 Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Gln Ala
151 Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe
166 Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu
181 Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe
196 Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro
211 Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
226 Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln
241 Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln

256 Pro Asp Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln
271 Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly
286 Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu
301 Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile
316 Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser (SEQ ID NO:277)

pmon16024.pep

1 Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu
16 Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp
31 Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn
46 Leu Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser
61 Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser
76 Ala Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly
91 Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr
106 Leu Glu Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly
121 Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser
136 Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Leu Gln
151 Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr
166 Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly
181 Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr
196 Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu
211 Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln
226 Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
241 Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Asp

256 Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe
271 Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly
286 Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His
301 Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp
316 Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala (SEQ ID NO:278)

pmon16025.pep

1 Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu
16 Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp
31 Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn
46 Leu Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser
61 Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser
76 Ala Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly
91 Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr
106 Leu Glu Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly
121 Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser
136 Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Leu Ala
151 Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly
166 Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr
181 Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile
196 Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
211 Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg
226 Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
241 Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Asp Met Ala

256 Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu
Leu
271 Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala
Ala
286 Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro
Glu
301 Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala
Pro
316 Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln (SEQ ID NO:279)

pmon16026.pep

1 Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
Leu
16 Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn
Asp
31 Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro
Asn
46 Leu Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala
Ser
61 Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro
Ser
76 Ala Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala
Gly
91 Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val
Thr
106 Leu Glu Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly
Gly
121 Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro
Ser
136 Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Glu
Leu
151 Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro
Ala
166 Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val
Ala
181 Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu
Arg
196 His Leu Ala Gln Pro Asp Met Ala Thr Pro Leu Gly Pro Ala
Ser
211 Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val
Arg
226 Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys
Ala
241 Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly
His

256 Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln
271 Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu
286 Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro
301 Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
316 Phe Ala Thr Thr Ile Trp Gln Gln Met Glu (SEQ ID NO:280)

pmon16027.pep

1 Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu
16 Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp
31 Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn
46 Leu Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser
61 Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser
76 Ala Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly
91 Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr
106 Leu Glu Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly
121 Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser
136 Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Gly Met
151 Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala
166 Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His
181 Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu
196 Ala Gln Pro Asp Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu
211 Pro Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile
226 Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr
241 Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu

256 Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu
271 Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu
286 Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu
301 Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala
316 Thr Thr Ile Trp Gln Gln Met Glu Glu Leu (SEQ ID NO:281)

pmon16028.pep

1 Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu
16 Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp
31 Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn
46 Leu Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser
61 Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser
76 Ala Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly
91 Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr
106 Leu Glu Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly
121 Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser
136 Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Ser Phe
151 Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Asp
166 Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe
181 Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly
196 Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His
211 Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp
226 Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly
241 Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu

256 Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu
271 Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp
286 Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro Thr
301 Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala
316 Gly Gly Val Leu Val Ala Ser His Leu Gln (SEQ ID NO:282)

MetAlaGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHis
LeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuAlaValArg
GluPheGlyGlyAsnMetAlaSerProAlaProProAlaAlaAspLeuArgValLeuSer
LysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHis
ProLeuProThrProValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThr
GlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGly
ValMetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeu
SerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuPro
ProGln (SEQ ID NO:284);

MetAlaGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeu
LeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThr
AlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysVal
ArgPheLeuMetLeuValGlyGlySerThrLeuAlaValArgGluPheGlyGlyAsnMet
AlaSerProAlaProProAlaAlaAspLeuArgValLeuSerLysLeuLeuArgAspSer
HisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProVal
LeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLys
AlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGly
GlnLeu (SEQ ID NO:285)